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(71) Applicants (for all designated States except US): BECTON, DICKINSON AND COMPANY [US/US]; Intellectual Property Department, 1 Becton Drive, MC 089, Franklin Lakes, NJ 07417-1880 (US). NOVOCELL, INC. [US/US]; 31 Technology Drive, Suite 100, Irvine, CA 92618 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): PRESNELL, Sharon, C. [US/US]; 11709 Old Creedmore Road, Raleigh, NC 27613 (US). ROBBINS, Neil [US/US]; 909 Kathryn Street, Cary, NC 27511 (US). HEIDARAN,

Mohammad [US/US]; 207 Painted Fall Way, Cary, NC 27511 (US). SPARGO, Catherine, A. [US/US]; 7103 Eastridge Drive, Apex, NC 27502 (US). HAALAND, Perry [US/US]; 8914 Laurel Springs Drive, Chapel Hill, NC 27516 (US). JURGENSEN, Stewart [US/US]; 7504 Valley Run Drive, Raleigh, NC 27615 (US). LATTA, Paul, P. [US]; Irvine, CA. SCHARP, David, W. [US]; Mission Viejo, CA. COUTTS, Margaret [/]; Irvine, CA.

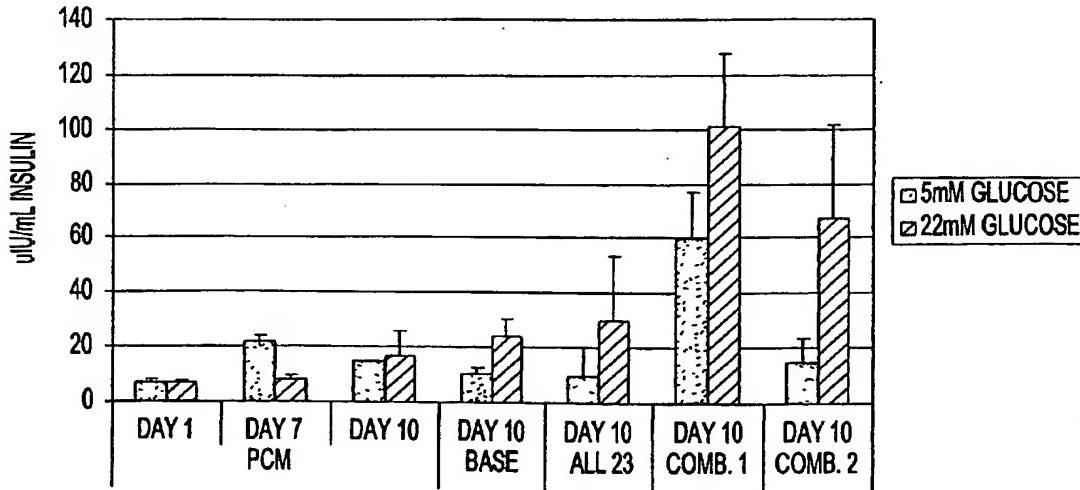
(74) Agent: HOBBS, Ann, S.; Venable LLP, P.O. Box 34385, 1201 New York Avenue, NW, Suite 1000, Washington, DC 20043-9998 (US).

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(54) Title: METHODS FOR *IN VITRO* EXPANSION AND TRANSDIFFERENTIATION OF HUMAN PANCREATIC ACINAR CELLS INTO INSULIN-PRODUCING CELLS



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(57) Abstract: This invention relates, e.g., to a method for expanding mammalian acinar cells, comprising culturing the cells in a cell culture system comprising a cell culture medium and a cell attachment surface, under conditions wherein the acinar cells undergo a 3-4 fold expansion together with transdifferentiation into a modified cell phenotype (IP cells) showing characteristics of acinar cells and liver cells. The invention also relates to a method for transforming these IP cells to insulin-producing cells *in vitro*, comprising culturing the cells in a novel, defined medium. Also disclosed are suitable culture media for performing these methods, isolated cells having the phenotype of IP cells and/or produced by these methods, and kits for performing the methods.



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**Methods for *in Vitro* Expansion and Transdifferentiation of Human  
Pancreatic Acinar Cells into Insulin-Producing Cells**

This application claims the benefit of provisional application 60/384,000, filed May 28, 2002, which disclosure is incorporated by reference in its entirety herein.

#### **BACKGROUND OF THE INVENTION**

##### **1. Field of the Invention**

[0001] The invention relates to compositions and methods whereby, e.g., human pancreatic acinar cells are cultured under conditions that support expansion and transdifferentiation into glandular epithelial cells and subsequently into insulin-producing cells.

##### **2. Background Information**

[0002] The potential benefits of taking insulin-producing cells from organ donors and transplanting them into insulin-dependent, Type I diabetic patients is clear. In the Edmonton clinical trials, many patients have lived free from the delivery of exogenous insulin for approximately 2 years after being transplanted with intact islets from organ donor sources. However, current technology requires two organ donor pancreata to generate a sufficient number of islets (about 1 million islets, comprised of about 1,000 cells each) to transplant into one diabetic patient for cellular therapy. Thus, there has been emphasis in the diabetes field to identify new sources of insulin-producing cells for transplantation. Many avenues are being explored, including expansion of islets after harvest and before transplantation and the generation of new islets from stem-like cells derived from the bone marrow, or from precursor cells located in the pancreas. The challenges presented by these approaches are related to maintenance of function of islets over long periods of culture, and of the relative rarity of stem-like cells that can be harnessed for insulin production from the bone marrow and pancreas. The ductular precursor stem-like cells derived from the pancreas are reported to be more efficient than bone-marrow derived cells at differentiation into insulin-producing cells, and this may reflect their site of origin (i.e., pancreas) where they are certainly exposed to many

differentiation signals related to the pancreatic microenvironment. The most abundant cell type in the pancreas is the acinar cell, which comprises about 85% of the pancreas. The acinar cells serve to produce and secrete digestive enzymes and, like islet cells, arise during development from the ductular cell compartment.

[0003] There have been reports that acinar cells, when cultivated *in vitro*, especially under conditions of stress, can undergo a 'transdifferentiation' into a cell type that resembles ductular cells, as determined by expression of CK19, CK7, and carbonic anhydrase (all reputed by the authors to be markers of duct cells) (Kerr-Conte, 1996; WO 02/29010 A2), Hall et al., 1992). Furthermore, Bouwens *et al.* (1998) have shown *in vivo*, in a model of pancreatic duct ligation, that acinar cells in the ligated portion of the pancreas undergo transdifferentiation into cells with a ductular phenotype. Further work has suggested that insulin-producing cells can be produced upon further differentiation of the duct cells in the ligated portion of the pancreas. The acinar cells are also reported to be of limited survivability in primary culture, with some culture conditions leading to loss of at least 50% of cells within a week. While primary duct cells have been demonstrated *in vitro* to convert into insulin-producing cells under some culture conditions (e.g. Bonner Weir, 2000, U.S. Pat. No. 6,011,647), there are no reports of cells that arose from acinar cells *in vitro* differentiating further to produce islet-like cells.

[0004] Prior to the development of the present system, primary pancreatic acinar cells were expanded **without differentiation** into insulin-producing cells, either in serum-containing medium (undesirable both because of the risk and the uncertainty associated with the use of serum), or in complex serum free media formulations. Likewise, primary pancreatic acinar cells have been transdifferentiated into insulin-producing cells **without expansion**, producing cells with an insulin-producing phenotype in small numbers. Furthermore, it has not been previously possible to obtain insulin-producing cells in good numbers using acinar cells as starting material.

[0005] Thus, there is a need for a simple cell culture system and method for rapidly generating large numbers of cells that can further differentiate into, *e.g.*, insulin-

producing cells, through expansion and differentiation of the abundant pancreatic acinar cells. Further, there is a need for a cell culture system and method for culturing and transforming such cells into insulin-producing cells. One cell culture system and related method disclosed herein allows a simple, one-step approach that generates expanded cultures that contain at least 80% intermediate progenitor cells that can give rise to insulin-producing cells. A second cell culture system and related method allows the further culturing of these intermediate progenitor cells or other glandular epithelial cells to obtain insulin-producing cells. Both IP cells and insulin-producing cells will be useful for cell-based therapies for the treatment of diseases such as diabetes.

#### SUMMARY OF THE INVENTION

[0006] The present invention provides compositions and methods whereby, *e.g.*, acinar cells can be cultivated successfully *in vitro*, undergoing a 3-4 fold increase in cell number over time, and giving rise to a cell population that co-expresses acinar and ductal markers early during the culture (2-3 days *ex vivo*), then ultimately (*e.g.*, about 7-8 days *ex vivo*) acquires a modified phenotype characterized by expression of some acinar-associated genes, as well as some liver-associated genes. The genes expressed by these modified cells at about 7-8 days *ex vivo* include, *e.g.*, ductular cytokeratins (CK7, CK8, CK18 and CK19), hepatic nuclear factor 1 (HNF1), alpha-1 antitrypsin, pi-glutathione s transferase (pi-GST), liver-specific (basic helix-loop-helix (bHLH) transcription factor, Thy-1, CCAAT/enhancer-binding protein (C/EBP)-alpha and C/EBP-beta. These cells exhibit little if any expression of the pancreas-associated genes carbonic anhydrase, cystic fibrosis transmembrane conductance regulator (CFTR), elastase and amylase. By "little if any" expression of a gene is meant herein that gene expression is generally undetectable under conventional methods, such as the hybridization and immunocytochemical methods described herein, but expression may be detected by extraordinarily sensitive methods, such as PCR-based analysis. This type of modified cell is referred to herein as an intermediate progenitor ("IP") cell. The expanded/transdifferentiated acinar cells (IP cells) can be produced using a general serum-containing media, or, in a preferred method, can be produced without serum on a surface comprising one or more extracellular matrix molecules (ECMs) in the presence of

one or more soluble active factors. ECMs can be presented in 2 dimensional or 3 dimensional culture systems in the presence of soluble active factors.

[0007] The IP cells generated from these cultures are expected to be useful directly in certain medical applications. For example, there is evidence that such cells may under certain conditions become functioning insulin-producing cells when implanted in diabetic patients. The cells can also be used for drug discovery and toxicity studies.

[0008] In addition, according to a further aspect of the invention, the IP cells can be cultivated further, in a serum-free medium composed of any standard serum-free base medium (DMEM:HamsF12, for example) with BSA and combinations of factors, including ECMs, small molecules, and growth factors. After 5-10 days of culture, the IP cells undergo additional steps of differentiation, culminating in the formation of cell aggregates that express pro-insulin and C-peptide. Challenge of these cultures with a high-glucose medium causes release of insulin and C-peptide into the medium, indicating the production in these cultures of functional islet-like cells.

[0009] Thus, in a first aspect, the present invention provides a cell culture system comprising a superior cell attachment surface that also stimulates cellular expansion, and a simple culture medium including effective amounts of one or more soluble active factors, or serum (*e.g.* fetal bovine serum), added to a base medium composition. The cell culture system will be particularly useful for primary culture of mammalian epithelial cells, particularly human epithelial cells. In a preferred embodiment the cell culture system is used for the expansion and transdifferentiation of primary acinar cells, especially human pancreatic acinar cells.

[00010] The cell attachment surface for this cell culture system is any surface to which the cells can attach and expand, including both 2 dimensional (*e.g.* plates, flasks, roller bottles, petri dishes, wells etc.) and 3 dimensional (*e.g.* scaffold) environments. Preferably the surface comprises at least one type of ECM, or a peptide fragment thereof. Cells may, in some circumstances, detach from these surfaces and form self-supporting

aggregates. Suitable fragments include peptides consisting of a sequence of three or more amino acid residues that are identical to any portion of the amino acid sequence of the ECM. Such fragments can be easily made and tested by means known to those of skill in the art. Most preferably the surface is a layer of collagen I. Many other surfaces known in the art are also suitable, such as Collagen VI, Collagen IV, Vitronectin, or Fibronectin. Collagen I is preferred due to ease and cost.

[00011] The base medium to which the soluble active factors are added may be any cell culture medium appropriate for growth and differentiation of epithelial cells. These include, but are not limited to, DMEM, Hams F12, MEM, M-199 and RPMI. The general requirements for such culture media and many suitable examples are known to those of skill in the art. To this base medium is added either serum (such as fetal bovine serum), or a stabilizing protein such as bovine serum albumin (BSA) along with effective amounts of soluble active factors. The medium is preferably serum-free.

[00012] Soluble active factors for the expansion and transdifferentiation of primary pancreatic acinar cells into IP cells include growth factors such as HGF receptor activators and EGF receptor activators. Preferred soluble active factors include one or more of EGF and Transforming Growth Factor- $\alpha$ , IGF1, HGF, betacellulin, prolactin and gastrin 1. HGF, EGF and/or Transforming Growth Factor- $\alpha$  are particularly preferred. Also preferred is the combination of IGF1 and betacellulin.

[00013] In one particularly preferred embodiment, the base medium contains a 1:1 mixture of DMEM and Hams F12. The base medium is completed with the addition of glutamine to a final concentration of ~4 mM, insulin (~0.1-10  $\mu$ g/ml, preferably ~0.01 mg/ml), transferrin (~0.5-10  $\mu$ g/ml, preferably ~0.0055 mg/ml), selenium (~0.25-5.0 ng/ml, preferably ~0.0067  $\mu$ g/ml of sodium selenite), and Epidermal Growth Factor (EGF) (~1-20 ng/ml, preferably ~10 ng/ml); this medium is hereafter referred to as pancreatic cell medium, or PCM. To this base medium formulation, up to ~20% Fetal Bovine Serum (or other serum), preferably between ~10 - ~15% fetal bovine serum, most preferably about 10% or up to about 15% fetal bovine serum) may be added, or, to create

a serum-free culture environment, the following components are added in place of serum: heat-inactivated bovine serum albumin (0.1–2%), Hepatocyte growth factor (HGF) (1-20 ng/ml), and/or Transforming Growth Factor Alpha (TGFA)(1-10 ng/ml). In addition, the medium may contain Betacellulin (0.5-20 ng/ml), Gastrin 1 (0.05-10 ng/ml), Prolactin (1.0–10 ng/ml), and/or IGF-1 (5-100 ng/ml). In particular formulations, greater or lesser amounts of these components may be added in order to achieve a formulation that is effective in supporting the expansion and transdifferentiation of the cells. Persons of skill in the art will appreciate that determining effective amounts of the components will require no more than routine experimentation.

[00014] By the use of this attachment surface and medium, the expansion and transdifferentiation of primary pancreatic cells with the desired phenotype is simplified greatly.

[00015] In a particularly preferred embodiment, the cell culture system is a combination of collagen I coated tissue culture surface (presented in a 2 dimensional or 3 dimensional form) and a serum-free medium containing BSA, insulin, transferrin, selenium, Hepatocyte growth factor (HGF), Epidermal Growth Factor (EGF) and Transforming Growth Factor Alpha (TGFA).

[00016] The cell culture system enables superior attachment *in vitro* of primary pancreatic epithelial cells for adherent culture compared to prior methods, while creating a cellular environment that promotes expansion of the epithelial component of primary pancreatic cultures with concomitant transdifferentiation of the acinar cells present in the starting material into IP cells, while minimizing emergence of undesired fibroblasts. Advantages of this culture system are ease of construction, few components needed, and that all components are readily available and easily used in the required manner.

[00017] The components of this aspect of the invention may be conveniently packaged in the form of a kit. The kit may include, for example, 1) a cell culture medium such as DMEM; 2) a serum-free medium supplement containing BSA, insulin, transferrin,

selenium, HGF, EGF and TGFA, in suitable amounts to yield the concentrations noted above in the completed medium; and 3) at least one collagen I coated substrate, such as a vessel for tissue culture (*e.g.*, dish(es) with at least one collagen-1 coated tissue culture surface), or collagen-1 coated inserts for use in culture dishes or other laboratory ware. The kit may also optionally include a tissue culture dish or other cell culture accessories and additional reagents that may be required to carry out epithelial cell culture and differentiation.

[00018] Culture systems consisting of scaffolds, collagen coated flasks or other vessels and serum-free base medium may be packaged along with the soluble active factors as a separate vial that would be added to the culture medium just prior to use. The active factor combination can be added to a variety of base media to accomplish the same end, *e.g.*, growth and differentiation of primary pancreatic acinar cells *in vitro*. Such culture systems should also be useful for other cell types, particularly glandular epithelial cells derived from other organs and tissues, including those from liver, pancreas, intestine, prostate, and breast.

[00019] The collagen I surface provides superior cell attachment (thereby increasing the number of cells that adhere during initial culture and thus enhancing culture efficiency), while the collagen I and the combination of soluble active factors (*e.g.*, HGF, TGFA and EGF) promote continued proliferation of cells over time, leading to an increase in cell number above what has been previously reported for primary pancreatic acinar cells. Furthermore, the expansion of the acinar cells is accompanied by a transdifferentiation in the majority of cells to an IP phenotype, which is potentially a therapeutically useful cell phenotype for the treatment of diseases such as diabetes. This likely occurs due to convergence of the intracellular signaling pathways associated with collagen I, HGF, TGFA and EGF, creating a synergistic response.

[00020] The cell culture system of the present invention has unexpected advantages over systems previously in use. Collagen I, IV, VI, Vitronectin and Fibronectin were expected to enhance cell attachment. However, other extracellular matrix molecules that yielded

equivalent attachment of cells during the initial 18 hours of culture did not promote consistent growth of the cells over time in the serum-free medium containing HGF/EGF/TGFA. The most efficient and cost-effective method of achieving cell expansion AND differentiation into IP cells is to utilize a collagen-I surface and a medium containing reduced serum (preferably less than 20%, more preferably less than 15%, 10%, or 5%, most preferably 2%).

[00021] Another aspect of the invention is a method for culturing mammalian epithelial cells comprising adding said cells to the cell culture system described above, and maintaining them at suitable temperature and atmospheric conditions. By "mammalian epithelial cell" is meant any cell of a tissue or organ with an epithelial cell phenotype, defined by the presence of expression of cytokeratins and often through the presence of markers that suggest a tissue-specific function (*i.e.*, epithelial cells of the skin make keratin, epithelial cells of the intestine make mucin, epithelial cells of the prostate make PSA). In a preferred embodiment, the cells are primary pancreatic cells, particularly human pancreatic cells. Suitable temperature for mammalian cells is usually in the range of about 37°C, but may be varied somewhat according to cell type. The atmosphere can be ordinary air, or other specialized mixtures of gasses suitable for maintaining cells, as will be familiar to persons of skill in the art. Expansion of pancreatic acinar cells can be maximized by decreasing the oxygen tension in the culture atmosphere to less than 21%, while transdifferentiation to IP cells can be enhanced by increasing oxygen tension to greater than 5%. A preferred range of oxygen tension is between about 5% and about 21%.

[00022] In a second aspect, the invention also provides methods and compositions for transforming glandular epithelial cells that have acquired expression of markers characteristic of an intermediate progenitor (IP) phenotype as described above into insulin-producing cells. By "glandular epithelial cell" is meant an epithelial cell that is a component of a gland. Glands are tissues that have a specific function related to secretion of key molecules – most organs in the body have glandular function (liver, intestine, pancreas, prostate, breast, pituitary, adrenal, kidney) whereby they produce and release

hormones, digestive enzymes, or other life-essential fluids. Glandular epithelial cells from endoderm-derived organs (*e.g.*, liver, intestine, pancreas) share many characteristics, including the ability to express many of the same genes. Particularly preferred are glandular epithelial cells from pancreas, for example acinar cells. As used herein, the terms "express" and "expression" generally refer to nucleic acids (*e.g.*, mRNAs) or to protein gene products that are detectable by standard immunocytochemical methods.

[00023] In this aspect, the invention provides a second cell culture system comprising a cell attachment surface and a culture medium that supports and promotes the transformation of glandular epithelial cells into insulin-producing cells. The cell attachment surface is similar to and may be identical to the attachment surface for expanding primary pancreatic acinar cells. It may be presented in the form of a flat surface coated on a vessel or in the form of a scaffold or other surface adapted for cell culture. It can be comprised of, or coated with, any composition that is capable of maintaining cells or supporting cell growth. In a preferred embodiment, it comprises at least one ECM, such as Collagen I, Collagen VI, Collagen IV, Vitronectin or Fibronectin. In a particularly preferred embodiment, the cell attachment surface is Collagen-I.

[00024] In this aspect, the invention provides a further culture medium comprising at least one differentiation promoting factor ("DPF") that promotes the transformation of glandular epithelial cells into insulin producing cells. The DPFs for the transformation of glandular epithelial cells into insulin producing cells can be one or more of Activin A, acidic FGF, basic FGF, C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit, Dexamethasone, Gastrin-Releasing Peptide, Glucagon-like Peptide-1 (GLP-1), Glucose, IGF1, IGF2, Insulin, Laminin, LIF, Met-Enkephalin, PDGFAA+PDGFBB, Prolactin, Sonic Hedgehog, Substance P, TGF-alpha, Trolox (alpha-tocopherol derivative), or VEGF. Preferred concentrations in culture medium of each of these 23 DPFs are listed in Table 1. Although in some cases one DPF is sufficient, preferably two or more factors are used. As many as all 23 of the factors may be used.

Table 1

Substance	Concentration (micrograms/ mL)
Activin A (human, recombinant)	0.0005
CGRP alpha, (Calcitonin Gene Related Peptide, rat)	0.1905
C natriuretic peptide) (human, porcine, rat: frag 32-53)(CNP)	0.10985
Cholera Toxin B Subunit, recombinant	0.0125
DEXamethasone (9 alpha-fluoro-16alpha-methylprednisolone)(hydrocortisone analogue)	0.002
FGF acidic (aFGF = FGF1), Recombinant Human	0.0025
GLP-1 (7-36) amide, human (Glucagon-Like Peptide 1)	0.033
Glucose (base should be 10ow; 0.9 ug/ml)	1.08
Insulin , human (low [ ] in base media 1 ug/ml)	9.5
LIF, human (leukemia inhibitory factor, human)	0.0025
PDGF AA + PDGF BB MIX	0.005
TGF alpha	0.001
Prolactin (human, recombinant)(a plasma growth hormone)	0.0012
Trolox (soluable Vitamin E) (C14H18O4)	0.625
GRP (Gastrin Releasing Peptide, Human)	0.143
IGF-1, recombinant human	0.0025
IGF-2, recombinant human	0.0025
Laminin	2.25
Met-Enkephalin (tyr-gly-glyl-phe-met)	0.003
Sonic Hedgehog (mouse, recombinant)	0.025
Substance P (full length) (H1875 is frag 1-4)	5
FGFb (=FGF2), human Recombinant	0.0025
VEGF	0.0025

[00025] In a preferred embodiment of this aspect of the invention, the culture medium comprises at least one (or as many as all 10) of the following differentiation promoting DPFs: C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit, Dexamethasone, Gastrin-Releasing Peptide, Laminin, Met-Enkephalin, PDGFAA+PDGFBB, Sonic Hedgehog, and Substance P.

[00026] In a preferred embodiment, the culture medium that promotes the transformation of glandular epithelial cells into insulin producing cells consists of a 1:1 mixture of DMEM and Hams F12 plus the components listed in Table 2. This medium is sometimes referred to herein as "Media or Medium G9."

Table 2

Factor	Substance	Concentration (Final) ug/ml
1 ANP	Atrial Natrluretic Peptide, Rat (28 amino acids)	0.1530
2 CCK-8-frag-amide	CCK8, Fragment 26-33 Amide (Cholecystokinin ) (Asp-Tyr(SO3H)-Met-Gly-Trp-Met-Asp-Phe-NH2)	0.0250
3 Caerulin sulfate	Caerulein (Pyr-Gin-Asp-Tyr(SO3H)-Thr-Gly-Trp-Met-Asp-Phe-NH2	0.0300
4 Cholera Toxin-B	Cholera Toxin B Subunit, recombinant	0.0125
5 Dex	DEXamethasone (9 alpha-fluoro-16alpha-methylprednisolone)(hydrocortisone analogue)	0.0020
6 FGF-7	FGF7 (KGF)	0.0025
7 GLP-1	GLP-1 (7-36) amide, human (Glucagon-Like Peptide 1)	0.0330
8 GRP	GRP (Gastrin Releasing Peptide, Human)	0.1430
9 Gastrin-1	Gastrin I Human	0.0000
10 Glucose	Glucose (base should be 10ow; 0.9 ug/ml)	1.0800
11 HGF	Hepatocyte Growth Factor (HGF) recombinant	0.0025
12 IGF-1	IGF-1, recombinant human	0.0025
13 IGF-2	IGF-2, recombinant human	0.0025
14 Insulin	Insulin (low I) in base media 1 ug/ml)	9.5000
15 Leu-Enkephalin	Leu-Enkephalin (tyr-gly-gly-phe-leu)	0.0030
16 Nicotinamide	Nicotinamide	610.0000

17	PTHRP-frag-1-34	pT II RP (Parathyroid Hormone Related Peptide (1-34), human)	0.2060
18	Progesterone	Progesterone	0.0030
19	Prolactin	Prolactin (human, recombinant)(a plasma growth hormone)	0.0012
20	Retinol acetate	Retinolc Acid (Vitamin A)	0.0250
21	SHH	Sonic Hedgehog (mouse, recombinant)	0.0250
22	Sodium selenite	Selenium (Selenous Acid, Na salt)	0.0250
23	Soybean trypsin Inhibitor	Trypsin Inhibitor, soybean (type I-S)	0.5000
24	TGF-beta sRII	TGF beta sRII (soluable receptor type 2)	0.0050
25	Transferrin	transferrin	2.7500
26	Trolox	Trolox (soluable Vitamin E) (C14H18O4)	0.6250
27	VIP	Vasoactive Intestinal Peptide (VIP), human	0.0665
28	aFGF	FGF acidic (aFGF = FGF1), Recombinant Human	0.0025
29	bFGF	FGFb (=FGF2), human Recombinant	0.0025
30	n-Butyric acid	n Butyric Acid, Sodium Salt	4.5400

[00027] The components of this aspect of the invention may also be conveniently packaged in the form of a kit. The kit may include, for example, 1) a cell culture medium such as DMEM, Hams F12, or a combination thereof; 2) a serum-free medium supplement containing: BSA and the DPFs Activin A, acidic FGF, basic FGF, C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit, Dexamethasone, Gastrin-Releasing Peptide, Glucagon-like Peptide-1 (GLP-1), Glucose, IGF1, IGF2, Insulin, Laminin, LIF, Met-Enkephalin, PDGFAA+PDGFBB, Prolactin, Sonic Hedgehog, Substance P, TGF-alpha, Trolox (alpha-tocopherol derivative), or VEGF, or two or more of these components in combination, in suitable amounts to yield the concentrations noted in Table 1 in the completed medium; and 3) tissue culture dish(es) with at least one collagen-1 coated tissue culture surface (or collagen-1 coated inserts for use in culture dishes or other laboratory ware). The kit may also optionally include a tissue culture dish and/or other cell culture accessories and additional reagents that may be required to carry out epithelial cell culture and differentiation. In other

embodiments, the kit may contain any of the media or media components discussed herein.

[00028] Culture systems consisting of scaffolds, collagen coated flasks or other vessels and serum-free base medium may be packaged along with the DPF(s) as a separate vial that would be added to the culture medium just prior to use. The DPF combination can be added to a variety of base media to accomplish the same end, e.g., growth and differentiation of primary pancreatic acinar cells *in vitro*. Such culture systems may also be useful for other cell types, particularly other epithelial cells derived from glandular tissues, including those from liver, pancreas, intestine, prostate, and breast.

[00029] The invention also provides a method for converting glandular epithelial cells into insulin-producing cells comprising culturing the glandular epithelial cells in the cell culture system described above. The method may further comprise removing the culture medium from the cell culture, re-feeding the cell culture with a serum-free medium with glucose, and measuring proinsulin production C-peptide production, or insulin release.

[00030] Furthermore, the invention provides an isolated population of insulin-producing cells containing cytoplasmic granules with immunodetectable proinsulin, insulin, and/or c-peptide that is derived from a population of cells of which a subset of cells expressed at least one marker associated with IP cells (e.g., expressed some acinar-associated genes, as well as some liver-associated genes, including, e.g., ductular cytokeratins (CK7, CK8, CK18 and CK19), HNF1, alpha-1 antitrypsin, pi-glutathione s transferase (pi-GST), liver-specific bHLH transcription factor, Thy-1, C/EBP-alpha and C/EBP-beta, and expressed little if any of the pancreas-associated genes carbonic anhydrase, cystic fibrosis transmembrane conductance regulator (CFTR), elastase and amylase).

[00031] By an “isolated” cell or population of cells is meant herein that the cell or cell population is removed from its original environment (e.g., the natural environment if it is naturally occurring), and isolated or separated from at least one other component with which it is naturally associated. For example, a naturally-occurring cell present in its natural living

host is not isolated, but the same cell, separated from some or all of the coexisting materials in the natural system, is isolated. Such cell or cell populations could be part of a cell culture or cell population, and still be isolated in that such culture or population is not part of its natural environment.

[00032] In one preferred embodiment, the insulin-producing cells are derived from glandular epithelial cells obtained from mammalian pancreas, such as primary acinar cells.

[00033] The data disclosed in the examples below are generated from freshly isolated human pancreatic cells. The expansion of primary human pancreatic cells in these conditions produces cultures with a mixed epithelial IP phenotype, suitable for *in vitro* studies of IP cells for a variety of purposes, and suitable for transplantation *in vivo* for cell therapy for the treatment of diseases such as diabetes. The IP cells generated by these methods may also be useful in the study of pancreatic cell biology, as normal controls in the study of pancreatic epithelial cancers, and to test the effects of drugs/compounds on normal pancreatic epithelial cells (ductal or acinar). Furthermore, the cells may be further cultured to yield insulin-producing cells as demonstrated below.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[00034] Figures 1A-D show microscopic images after treatment of starting material with antibodies to amylase (Fig. 1A), insulin (Fig. 1B), and CK19 (Fig. 1C) and the composition of the cell pellet of freshly isolated primary human pancreatic cells (Fig. 1D).

[00035] Figure 2 shows growth curves constructed from primary human pancreatic cultures grown in commercial medium (with serum) or in the described pancreatic cell medium (PCM) with serum.

[00036] Figure 3 shows a comparison of cell expansion in the base medium composition described vs. base medium + soluble growth factors (serum-free formula) vs. base medium + fetal bovine serum.

[00037] Figures 4A-B shows the effect of different culture surfaces on total cell number (Fig. 4A) and cell phenotype (Fig. 4B) after expansion.

[00038] Figures 5A-B show a comparison of cell phenotype after expansion in serum-containing (5A) and serum-free (5B) medium containing all soluble active factors.

[00039] Figure 6 shows high power images of cell cultures expanded in various conditions, including serum-free base media supplemented with 3 soluble active factors, HGF, EGF & TGFA. Note epithelial morphology.

[00040] Figure 7 shows a demonstration of growth of IP cells on ECM-coated surfaces as determined by metabolic activity assay over time. Note superior growth when Collagen I surface is combined with the media formulation described herein, yielding results superior to the combination of Matrigel and commercial media with serum.

[00041] Figure 8A (upper left) shows expression of amylase by acinar cells after two days of culture (red staining), Figure 8B (lower left) shows expression of CK19 (green staining), Figure 8C (right) shows an overlay of the two images, showing co-expression (yellow) in a large proportion of cells.

[00042] Figure 9 shows changing phenotype of primary acinar cells in culture over 5 days. Amylase is red, CK19 is green. Note appearance of yellow (amylase + CK19) on Day 2 and 3.

[00043] Figures 10A and 10B show primary human pancreatic cells that were expanded in serum-containing medium on Collagen I coated surface. Images were analyzed to

determine total cells (Figure 10A, blue nuclei) and total positive cells (Figure 10B, blue nuclei surrounded by green staining for CK19).

[00044] Figure 11 shows light microscopic (200X) appearance of pancreatic acinar cells cultured on a collagen I surface with all DPFs (Activin A, 0.5 ng/ml; acidic FGF, 2.5 ng/ml; basic FGF, C-Natriuretic Peptide (CNP), 0.11  $\mu$ g/ml; Calcitonin Gene Related Peptide, 0.19  $\mu$ g/ml; Cholera Toxin B Subunit, 12.5 ng/ml; Dexamethasone, 0.002  $\mu$ g/ml; Gastrin-Releasing Peptide, 0.143  $\mu$ g/ml; Glucagon-like Peptide-1 (GLP-1), 0.033  $\mu$ g/ml; Glucose, 1.08  $\mu$ g/ml; IGF1, 0.0025  $\mu$ g/ml; IGF2, 0.0025  $\mu$ g/ml; Insulin, 9.5  $\mu$ g/ml; Laminin, 2.25  $\mu$ g/ml; LIF, 0.0025  $\mu$ g/ml; Met-Enkephalin, 0.0030  $\mu$ g/ml; PDGFAA+PDGFBB (0.0050  $\mu$ g/ml: 0.0025  $\mu$ g/ml of PDGFAA + 0.0025  $\mu$ g/ml PDGFBB); Prolactin, 0.0012  $\mu$ g/ml; Sonic Hedgehog, 0.025  $\mu$ g/ml; Substance P, 5.0  $\mu$ g/ml; TGF-alpha, 0.0010  $\mu$ g/ml; Trolox (alpha-tocopherol derivative), 0.625  $\mu$ g/ml; and VEGF, 0.0025  $\mu$ g/ml).

[00045] Figure 12A (top right panel) shows immunocytochemical analysis with CK19 antibodies (green).

[00046] Figure 12B (lower right panel) shows immunocytochemical analysis with C-peptide antibodies (red).

[00047] Figure 12C (left panel) shows an overlay image demonstrating the colocalization of CK19 and C-peptide (orange). Blue portions are DAPI stained nuclei.

[00048] Figure 13A shows insulin release upon glucose challenge in IP cells that have not been detached and relocated (subcultured) during the growth and differentiation process.

[00049] Figure 13B shows insulin release upon glucose challenge in IP cells that have been subcultured according to Example 10.

[00050] Figure 13C shows C-peptide release upon glucose challenge in IP cells that have not been subcultured according to Example 10.

[00051] Figure 14 shows the Insulin/DNA ratio in subcultured and nonsubcultured cells that are treated with Combinations 1, 2 and 3 of DFP media, as described in Example 11.

[00052] Figure 15 shows insulin release in response to base level glucose (5 mm) and a glucose challenge (22mm) over 10 days of culture in PCM and DPF media, as described in Example 13.

[00053] Figure 15A shows insulin release in response to base level glucose (5 mm) and a glucose challenge (22mm) over 14 days of culture in PCM and DMG9 media, as detailed in Example 14.

[00054] Figure 16 is a graphical representation of the characteristics of the 17 classes of genes shown in Table 6, as indicated in the last column of the Table, as detailed in Example 14.

#### DETAILED DESCRIPTION OF THE INVENTION

[00055] In describing preferred embodiments of the present invention, specific terminology is employed for the sake of clarity. However, the invention is not intended to be limited to the specific terminology so selected. It is to be understood that each specific element includes all technical equivalents, which operate in a similar manner to accomplish a similar purpose. Each reference cited here is incorporated by reference as if each were individually incorporated by reference.

[00056] The following abbreviations are used:

BSA: bovine serum albumin

BMP Bone Morphogenetic Protein

bHLH: basic helix loop helix

DMEM: Dulbecco's Modified Eagle's Medium

TGF $\beta$ 1: Transforming Growth Factor  $\beta$ 1

ECM: extracellular matrix molecules; naturally occurring proteins produced by cells of a tissue that provide structural support as well as a source of cellular signals related to adhesion. Examples are collagen, vitronectin, fibronectin, laminin.

EGF: Epidermal Growth Factor

Hams F12: Ham's Nutrient Mixture F12

HGF: Hepatocyte growth factor

HNF-1: Hepatic nuclear factor 1

IGF1: Insulin-like growth factor 1

IGF-II: Insulin-like growth factor 2

IP cells: Intermediate progenitor cells derived from an epithelial cell, such as, e.g., a pancreatic acinar cell or a liver cell, wherein the derived cells express some acinar-associated genes, as well as some liver-associated genes, including, e.g., cytokeratins (CK7, CK8, CK18 and CK19), HNF1, alpha-1 antitrypsin, pi-glutathione s transferase (pi-GST), liver-specific bHLH transcription factor, Thy-1, C/EBP-alpha and C/EBP-beta, and express little if any of the pancreas-associated genes carbonic anhydrase, cystic fibrosis transmembrane conductance regulator (CFTR), elastase and amylase).

PDGF-A: Platelet derived growth factor alpha

PDGF-B: Platelet derived growth factor beta

TGFA, TGF- $\alpha$ : Transforming Growth Factor  $\alpha$

[00057] As used herein, the term "culture system" is intended to mean a system for growing and/or differentiating cells in culture, which comprises a cell attachment surface, preferably one that also stimulates cellular expansion, and a culture medium, which includes effective amounts of one or more factors, or serum (e.g. fetal bovine serum), added to a base medium composition.

[00058] When referring to active soluble factors and DPFs herein, "effective amount" means an amount that either alone or in combination with other included factors is

effective in promoting either expansion and differentiation into IP cells, or into insulin-producing cells, as applicable.

## EXAMPLES

### I. Expansion and transdifferentiation of primary acinar cells into glandular epithelial cells (Culture Phase I)

#### Materials and methods:

[00059] **Starting Material:** Primary human pancreatic acinar cells are collected as waste from standard COBE gradient preparation of islet cells for transplantation (Lake et al., 1989). After density gradient centrifugation, the islets are present as a layer between 1.063 density and 1.10 density, and the remaining cells are collected as the pellet that sediments to the bottom of the gradient based on density. Approximately 48 hours after collection of the cells at the transplant center are received by the inventors in non-tissue-culture treated polystyrene flasks and are suspended in RPMI + 10% fetal calf serum at a density of approximately 2.0 million cells/ml. Cell number and viability is assessed by trypan blue exclusion and enumeration on a hemacytometer by light microscopic observation.

[00060] **Phenotypic Evaluation of Starting Material.** A preparation of starting material was formalin fixed and paraffin-embedded as a cell pellet about 24 hours after initial harvest of the pancreatic cells. Paraffin sections were prepared, placed on slides, and subjected to immunocytochemical analysis with antibodies to insulin (Biogenex, San Ramon, CA), CK19 (Biogenex), and Amylase (Biogenex). A minimum of (3) sections per sample were assessed with each marker. All antibody staining was carried out according to the manufacturer's suggestion with pre-diluted commercial antibodies. For CK19, a 3 minute treatment with pepsin enzyme (Biogenex) preceded the blocking step for the purpose of antigen retrieval. Briefly, the sections were rehydrated through graded ethanols, followed by a 15 minute incubation in phosphate buffered saline (PBS) without calcium and magnesium. Protein Blocker (Biogenex) was added for 30 minutes prior to addition of primary antibodies. After (3) 5-minute washes, biotinylated secondary

antibody (Biogenex) was added at a 1:100 dilution and sections were incubated for 30 minutes at room temperature. After (3) 5-minute washes, Alexa488 or Alexa-596-conjugated StreptAvidin (Molecular Probes, Eugene, Oregon) was added for fluorescent visualization. For each slide, a minimum of (3) 200x images were captured using a Nikon fluorescent microscope fitted with a SPOT camera (Diagnostic Systems, Inc., Webster, TX). The images were assessed quantitatively using image analysis software (MetaMorph/Universal Imaging Corporation, Downingtown, PA) to determine relative fraction of insulin-positive, CK19+, and amylase+ cells. Insulin+ cells are the beta cells of the islets, CK19+ cells are the primary ductal cells, and amylase+ cells are the acinar cells (see Example 1).

#### **Example 1: Characterization of cell culture conditions**

##### **A. Serum-free medium**

[00061] Freshly isolated primary human pancreatic cells were collected as a pellet from a COBE cell separator, fixed in formalin, paraffin-embedded, sectioned, and analyzed with antibodies to amylase, CK19, and Insulin. Images (Figures 1A and 1B) were collected on a Universal Imaging System (Universal Imaging Corporation) and analyzed with MetaMorph Software. This cell pellet (Figure 1C) was comprised of 1.0% insulin+ cells (beta cells of the islet), 5.8% CK19+ cells (primary ductal cells), and 93.2% amylase+ and unlabeled (acinar cells and other cell types).

[00062] Primary human pancreatic cells were then seeded at  $10^4$  or  $10^5$  cells/ cm<sup>2</sup> onto tissue culture treated polystyrene in either DMEM commercial medium plus 10% fetal bovine serum or in PCM plus 10% fetal bovine serum. Replicate cultures were harvested at 3 day intervals via trypsinization and live cells (as determined by trypan blue exclusion) and enumerated on a hemocytometer. The results (shown in Figure 2) demonstrate that the (serum-containing) medium formulation described herein is superior to commercial media formulation for growth and maintenance of primary pancreatic cells. Figure 3 compares the results of expanding the cells for 6 days in base medium, base medium plus all of the soluble active factors [HGF, ~1~20 ng/ml, preferably ~5.0 ng/ml; TGFA, ~1~10 ng/ ml, preferably ~2 ng/ml; Betacellulin, ~0.5~20 ng/ml,

preferably ~10ng/ml; Gastrin 1, ~0.05~10 ng/ml, preferably ~0.06 ng/ml; Prolactin, ~1.0~10 ng/ml, preferably ~2.4 ng/ml; and IGF1, ~5~100 ng/ml, preferably ~ 5 ng/ml] and base medium plus 10% serum. The serum-free media formulation meets/exceeds expansion provided by media + serum.

[00063] The cell expansion experiment was repeated essentially as above, except that the base medium was supplemented with only three of the soluble active factors: TGF, HGF, and EGF. Figure 6D compares the results of expanding the cells in the various media; Figures 6A, 6B and 6C show high power images of the cell cultures expanded under the various media conditions.

### B. ECM Surfaces

[00064] The attachment of primary human pancreatic cells was evaluated by counting the number of attached cells vs. the number of cells initially seeded on a panel of ECM surfaces comprised of Collagen I ( $1 \mu\text{g}/\text{cm}^2$ ), Fibronectin ( $3 \mu\text{g}/\text{cm}^2$ ), Laminin ( $2 \mu\text{g}/\text{cm}^2$ ), Vitronectin ( $1 \mu\text{g}/\text{cm}^2$ ), Matrigel ( $1 \mu\text{g}/\text{cm}^2$ ), Human ECM ( $1 \mu\text{g}/\text{cm}^2$ ), or Poly-D-Lysine ( $3 \mu\text{g}/\text{cm}^2$ ). In one condition, a mixture of Collagen IV, Laminin, and Fibronectin was utilized. ECMs were placed into solution at the above concentrations and allowed to coat tissue culture-treated polystyrene surfaces according to manufacturer's suggestions of 1 hour at room temp. Excess ECM solution was then removed and surfaces were rinsed twice in water. Just before seeding cells, the water was aspirated, then cells were seeded onto the ECM surface at a density of  $1 \times 10^5 \text{ cells}/\text{cm}^2$  in growth medium (PCM) composed of DMEM:HamsF12 mixture (1:1) with 4mM glutamine, 1x ITS supplement (GIBCO 51500-056), 10% Fetal Calf Serum (Inactivated, Qualified, GIBC 26140-079), and 10 ng/ml Epidermal Growth Factor (EGF) (BD 4001). Cells were seeded onto tissue-culture polystyrene surface as a control. After 18 hours, unattached cells were washed away and remaining attached cells were re-fed with PCM and allowed to grow for 7 days prior to evaluation. Cultures were fixed in 10% formalin and subjected to immunocytochemistry with antibodies for CK19 and Amylase as described previously to determine phenotypic composition. Cells were counterstained with DAPI fluorescent blue nuclear stain to visualize individual cell nuclei for cell counting. The metabolic

activity of cells subjected to the various conditions was determined by an MTS assay. Viable cells were measured using the MTS assay (Promega CellTiter 96 Aqueous One Solution Cell Proliferation Assay), a colorimetric method for determining the number of viable cells in proliferation or cytotoxicity. The results of this analysis are shown in Figure 7.

**Example 2: Further studies with ECM surfaces and various media components**

[00065] Primary pancreatic cells, composed of >90% non-islet/non-duct cells, were plated onto various coated surfaces at a density of 28,900 cells/well ( $10^5$  cells/cm $^2$ ). Unattached cells were washed off after 18 hours, and cultures were re-fed and allowed to grow for 8 days. Cultures were fixed in formalin (10%) and subjected to phenotypic analysis with antibodies to CK19 and Amylase. The results are shown in Figure 4A-B. While Collagens I, IV, Laminin, Fibronectin, and Matrigel provide a suitable surface for cell attachment and expansion, maintenance of acinar (amylase+) phenotype along with the presence of an increased proportion of cells with a glandular epithelial phenotype (CK19+) was superior on Collagen I. More than 50% of cells analyzed expressed amylase and more than 50% of cells analyzed expressed CK19, suggesting that a subpopulation of cells in these experimental conditions express both markers.

[00066] Tissue culture-treated polystyrene culture surfaces were coated with Collagen I as described above. Tissue culture medium (PCM) was prepared as described above. In some cases, serum was replaced with Fraction V BSA (99% pure, heat inactivated, Sigma), along with combinations of soluble growth factors, including IGF1, IGF2, betacellulin, HGF, EGF, and TGF-alpha. Optimal seeding density is between  $10^4$  and  $10^5$  cells/cm $^2$ , as demonstrated in Example 3. Cells were seeded onto collagen-coated flasks (150 cm $^2$ ) at  $1.5 \times 10^6$  cells/flask in PCM. After an ~18hr attachment period, unattached cells were washed away with gentle aspiration/rinse, followed by re-feeding with fresh medium. Cultures were monitored over time by metabolic assay (MTT) and by trypsinization and cell counting, to establish cell number (see example 3). Cell phenotype at the end of the culture period was assessed as follows: small-scale cultures were set up simultaneously in 96-well plates. At the end of the culture phase, monolayer cells were

fixed in 10% formalin for a minimum of 1 hour. After formalin was removed and monolayers were rinsed, cultures were subjected to immunocytochemistry as described in previous section for CK19, amylase, insulin, and vimentin (a marker of fibroblasts). The relative fraction of CK19+ cells was determined by quantitative image analysis as described above (see Example 4). After formalin was removed and monolayers were rinsed, cultures were subjected to immunocytochemistry as described in previous section for CK19 and vimentin (a marker of fibroblasts). Cells were also stained with amylase antibodies, but did not produce positive results due to release of digestive enzymes, such as amylase, by the cells over time in culture. The relative fraction of CK19+ cells was determined by quantitative image analysis as described above (see example 4). Acquisition of ductal markers by acinar cells was verified by demonstrating concomitant expression of CK19 and amylase in cell subpopulations during days 2-3 of culture (see example 5). For these experiments, CK19 primary antibodies were reacted with formalin-fixed cell cultures, followed by visualization with Alexa488-conjugated Goat anti-mouse IgG (Molecular Probes). Then, cells were subjected to a blocking step (Protein Blocker, BioGenex), followed by application of the second primary antibody (anti-amylase). Visualization of the amylase was accomplished by application of Alexa594-conjugated Goat Anti-Mouse IgG. Images were collected as described above. At the end of a 7-day culture period in the conditions described herein, between 65-90% of the cells in the culture express CK19, while less than 20% express vimentin (see example 6). Variations in the relative proportion of CK19+ cells probably reflect heterogeneity due to age, gender, and other unique characteristics of individual patients.

### **Example 3: Density of cell seeding**

[00067] Primary pancreatic cells were seeded at (3) densities on tissue-culture treated polystyrene dishes (60mm) and fed with PCM. Light microscopic observations were made daily. At the 24-hour timepoint, dishes were sacrificed and stained with trypan blue to assess viability. The results are shown in Table 3.

TABLE 3

Seeding Density	At 24 Hours:	At 48 Hours:	After 3 days Growth:
$10^4$ cells/cm <sup>2</sup>	Most cells attached, trypan blue negative (live)	Mitotic Figures present (light microscopy)	Epithelial monolayer forming
$10^5$ cells/cm <sup>2</sup>	Most cells attached, trypan blue negative (live)	Mitotic Figures present (light microscopy)	Epithelial monolayer forming
$10^6$ cells/cm <sup>2</sup>	Some cells attached, most are trypan blue positive (dead)	Few Mitotic Figures present (light microscopy)	Cells are detached; some fibroblasts present

[00068] Example 4. Cells were grown on a Collagen I surface, at 37°C in 21% oxygen, in PCM medium or in base medium with 2 % BSA, 2 ng/ml TGF- $\alpha$ , 10 ng/ml EGF, and 10 ng/ml HGF. After 7 days, cultures were fixed in 10% formalin and subjected to immunocytochemical analysis with fluorescent detection, followed by automated image collection and analysis. The results are shown in Figures 5A and 5B. Fibroblast (vimentin+) fraction, glandular epithelial cell fraction (CK19+), and fraction of unlabeled cells (Other) are similar after expansion. This suggests that replacement of serum with the serum-free medium maintains fraction of CK19+ cells without overgrowth of fibroblasts as compared to cells grown in serum-containing media.

[00069] Example 5. Primary pancreatic acinar cells were cultured for several days in a 1:1 ratio of DMEM and HamsF12, with 10% fetal bovine serum, 0.01 mg/ml insulin, 0.0055mg/ml transferrin, 0.0067 $\mu$ g/ml sodium selenite, 10 ng/ml EGF, 4mmol/liter glutamine and antibiotics. After 2 days of culture (4 days *ex vivo*), expression of amylase by the acinar cells is still strong (Figure 8A, upper left panel, red staining) as determined by immunocytochemistry. Expression of CK19 is also apparent (Figure 8B, lower left panel, green staining). Overlay of the two images (Figure 8C) demonstrates clear co-expression of amylase and CK19 in a large proportion of the cells, indicating that an

intermediate cell exists from active conversion of amylase+ acinar cells to an amylase+/CK19+ mixed acinar/ductal phenotype (AD cells). Daily evaluation of cultures (Figure 9) demonstrated that onset of CK19 expression begins around Day 2 of culture and by Day 5 cultures have lost most immunodetectable amylase expression and CK19 expression is prevalent.

[00070] **Example 6.** After 7 days of growth in PCM / Collagen I surface, cells were fixed, stained with antibodies to CK19, and counterstained with nuclear DAPI. Total cell number was evaluated by automated image analysis (Figure 10A left panel, blue-stained cell nuclei), while CK19+ cells were counted (Figure 10B, right panel, green-stained cell cytoplasm). Of 378 total cells, 342 were immunopositive for CK19 (90%). After approximately 7 days of culture using conditions described herein, the acinar cells have concrete ductular characteristics, now referred to as IP cells. For most primary human cultures, more than 80% of cells in the culture after about 7 days express markers such as CK19 that are associated with ductular cells from a variety of tissues.

[00071] **Example 7: Gene Expression Analysis of 7-Day Cultures (IP Cells).**

Two independent IP cell cultures were subjected to Clontech 8K Atlas Gene Array analysis. IP cells were obtained by culturing primary acinar cells in a cell culture system comprising PCM and a Collagen I surface. Monolayer cultures were rinsed 2x with PBS, then detached from the flasks with 0.25% trypsin. Cells were pelleted by centrifugation at 1,200 RPM for 3 minutes in a swinging bucket centrifuge. Cell pellets were resuspended and washed 2x in PBS before a final centrifugation at 1,200 RPM for 3 minutes as described above. The supernatant was discarded and gently aspirated to remove as much liquid as possible from the cell pellet, which was then quick-frozen in a dry-ice/ethanol bath and stored at -80°C until transfer to BD Clontech where gene expression analysis was performed, using conventional techniques.

[00072] Labelled P-33 cDNA probes were prepared from the 30 µg of total RNA from each sample by first enriching for poly A + RNA using a streptavidin-magnetic bead separation method that is part of the Atlas Pure Total RNA Labeling system. The labeled

probes from each sample were hybridized with the plastic human 8 K gene arrays for about 16 hours, the arrays were washed and imaged according to the Atlas array protocols. The Atlas image 2.7 software was used to align array images with the array grid template and to exclude false background signals or false signals due to strong signal bleedover. The transcript signals were then extracted from these aligned arrays using the Atlas Image 2.7 software and further statistical analysis of the changes in gene expression were performed.

[00073] In general, mRNA transcription was assayed, by hybridization to suitable oligonucleotide probes. In a few cases, e.g., for CK19 and amylase, the protein expression product was measured, using conventional methods of immunohistochemistry. A summary of the expression by these cell populations of a selected set of genes is presented in Table 4. Table 4 contains a list of genes expressed in IP cells and a comparison of expression patterns in primary acinar cells and primary ductal cells. Gene products identified as "+" were expressed; those identified as "++" were strongly expressed. Gene products designated ® are found in regenerating pancreas.

TABLE 4:

Gene	IP Cells	Primary Ductal Cells	Primary Acinar Cells
Aquaporin 1	+	++(mRNA)/+(protein)	0
Aquaporin 5	++	+(mRNA)/-(protein)	
Aquaporin 8	+	-	+
Insulin Receptor Substrate-2	+	++ ®	
Protein Kinase B (AKT)	0	+	+
Calpain (mu)	++	++	++
CFTR (Cystic Fibrosis Transmembrane Conductance Regulator)	0	0	0
Claudin 2	nd	++	
Claudin 3	+	+	+
Claudin 4	+	+	+
Claudin 5	nd	-	++
Carbonic Anhydrase II	0	0	0
Inositol 1,4,5 triphosphate	++	-	++
Rc, Type 3	+	++	+
MUC-1			

MUC-6	++	+	
Cytokeratin 7	++	++	
Cytokeratin 8	++	+	
Cytokeratin 18	+	+	
Cytokeratin 19	+	++	
alpha v integrin	0	+	
alpha 3 integrin	++	n/a	
beta 3 integrin	0	+	
beta 4 integrin	+	n/a	
beta 5 integrin	0	+	
fibronectin	0	+	
collagen IV	+	+	
vitronectin	0	+ ®	
MMP2	0	Trace	
MMP9	+	Trace	
TIMP1	++	Trace	
TGF-alpha	Trace	++ ®	
Gastrin	0	++ ®	
ICAM-1	0	0	
ICAM-2	0	0	
ICAM-3	0	0	
Pancreatitis Associated Protein (PAP)	++	+ ®	Trace
Reg-1	+	0	Trace
pyrimidinergic receptor P2Y	+	+	
Syndecan	+	+ (low)	Trace
Glutathione S Transferase - pi	+	+	

II. Transformation of glandular epithelial cells into insulin producing cells – Generating insulin-producing cells by differentiation of IP cultures (Culture Phase II)

[00074] IP cultures can be utilized to generate insulin-producing cells by placing the cells in a second phase of culture that includes a surface, such as Collagen I, that promotes attachment of the IP cells combined with a defined medium formula that lacks serum but contains combinations of the following differentiation promoting factors: Activin A, acidic FGF, basic FGF, C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit, Dexamethasone, Gastrin-Releasing Peptide,

Glucagon-like Peptide-1 (GLP-1), Glucose, IGF1, IGF2, Insulin, Laminin, LIF, Met-Enkephalin, PDGFAA+PDGFBB, Prolactin, Sonic Hedgehog, Substance P, TGF-alpha, Trolox (alpha-tocopherol derivative), and VEGF. In the following examples, the base medium is composed of a 1:1 mixture of HamsF12 and DMEM with antibiotics and 0.2% Bovine Serum Albumin (Fraction V, heat inactivated 99% pure). In one example (Combination 1), the base medium contained Cholera Toxin B, Dexamethasone, GRP, GLP-1, Glucose, IGF-1, IGF-2, Insulin, Prolactin, Sonic Hedgehog, Trolox, aFGF, and bFGF. In another example (Combination 2), the base medium contained Activin A, CGRP-alpha, CNP, Glucose, GLP-1, IGF-2, Insulin, LIF, Met-Enkephalin, Prolactin, Sonic Hedgehog, aFGF, and vEGF. In a third example (Combination 3), the base medium contains Activin A, CGRP-alpha, Cholera Toxin B, Dexamethasone, Glucose, GLP-1, Insulin, LIF, Laminin, Met-Enkephalin, PDGFAA/BB, Sonic Hedgehog, Substance P, TGF-alpha, aFGF, and VEGF. The concentrations of these media supplements are listed in Table 1.

[00075] AD cells were placed into culture by either: 1) trypsinizing the cells from the surface on which they were generated, and redistribution onto a fresh attachment-promoting surface at a density of ~5 x 10<sup>4</sup> cells/cm<sup>2</sup>, or 2) removing the medium, washing 2x in PBS to remove traces of old medium, and cultures re-fed with the new medium (described above) containing differentiation promoting factors. Cells are cultured for a period of 4-10 days at 37°C and 21% oxygen. On Day 5, half of the medium is removed and replaced with an equal volume of fresh medium containing differentiation promoting factors.

#### **Phenotypic Analysis of IP cells After Differentiation Culture.**

[00076] Morphological assessment of IP cells cultured in differentiation conditions described above was captured by light microscopy (see Example 8, below). The cellular phenotype of the cells comprising these cultures was assessed by immunocytochemistry as described above using monoclonal antibodies to vimentin, pro-insulin, C-peptide, MUC-1, and CK19 (See Example 10, below). Briefly, cultures were fixed with 10%

formalin for 1 hour at room temperature, then washed with PBS and subjected to immunocytochemical protocol. (See Example 9, below).

**Functional Analysis of IP cells After Differentiation Culture.**

[00077] The ability of the aggregated cell clusters to release insulin and C-peptide was assessed by subjecting the cultured cells to a glucose challenge as follows. Cells that had been cultured in differentiation medium for 7-10 days were washed 3x in PBS, then re-fed with either 1) base medium (described above) with 5mM Glucose, or 2) base medium with 22mM glucose. After 18 hours, the cell-conditioned medium was collected and subjected to ELISA analysis for insulin and C-peptide release (Diagnostic Systems Laboratories (DSL)). ELISAs were conducted using the standard range assay procedure according to manufacturer's specifications. Plates were incubated on a shaker during the assay and results were read in a Tecan spectrophotometric plate reader. Total ng of insulin or C-peptide per well were calculated for each media condition, for both 5mM glucose media and 22mM glucose media (See Example 10).

[00078] Example 8. Pancreatic acinar cells were cultured in Base Medium + ITS + Serum (10%) for 1 week, then trypsinized (treated with 0.25% Trypsin without EDTA for 10 minutes at 37°C) and transferred to a fresh collagen-1 coated surface and placed in a medium containing all 23 DFPs listed. Over a period of 3-5 days, the cells readily formed three-dimensional pod-like structures, clearly observable by light microscopy (Figure 11). Some larger pods detached from the culture surface after about 4-6 days in culture, and remained viable, as determined by trypan blue exclusion. The pod-like structures were hypothesized to be aggregations of insulin-producing cells, and subjected to further analysis as described below.

[00079] Example 9. Pod-like structures, generated the same manner as described in the previous example, were fixed in 10% formalin and subjected to immunocytochemical analysis first with CK19 monoclonal antibodies, then with C-peptide monoclonal antibodies, as described above. Figure 12A shows a group of cells (DAPI stained nuclei are blue), some of which are immunopositive for CK19 (green staining). Figure 12B

shows the same group of cells, many of which are positive for C-Peptide, which is produced when the proinsulin molecule synthesized within the cell is cleaved to yield mature insulin; the C-peptide stained cells are red, with a typical granular staining of the cytoplasm. Figure 12C shows a higher power overlay image, demonstrating colocalization of CK19 and C-peptide in a small subset of cells. Co-stained cells appear yellow-orange on the overlay image.

[00080] **Example 10.** Cells cultured in base medium (negative control), or in Combinations 1, 2 and 3 of the differentiation promoting media, were evaluated for their ability to release insulin and C-peptide into the culture medium. In addition, we assessed whether increasing concentrations of glucose led to the release of a greater quantity of insulin and C-peptide, indicating an islet-like functionality. First, the cells were cultured for 1 week in base medium + EGF(10 ng/ml) + ITS + 10% fetal bovine serum (PCM). Then, cells were either subjected to a wash and medium change (non-subcultured), or to a wash, trypsinization/detachment, reseeding, and medium change. Replicate cultures were re-fed with either base medium (serum-free), fresh PCM, or one of the three combinations of differentiation promoting media (all serum-free). After 10 days, differentiation media were removed, cultures were washed 3x with PBS, then re-fed with serum-free base medium containing either 5mM glucose or 22mM glucose (final concentration). After 18 hours, the conditioned media were collected and subjected to ELISA analysis with antibodies to either Insulin or C-Peptide (DSL laboratories). Figures 13A, 13B and 13C, respectively, show insulin release by nonsubcultured cells, and insulin release and C-peptide release in response to glucose challenge. Since some of the cultures contain insulin, and cells can take insulin up from the medium, production of C-peptide is an important confirmation that the cells are synthesizing insulin *de novo* from the synthesis and processing of proinsulin. Furthermore, the production of insulin and C-peptide is increased in most cases with increasing glucose concentration, suggesting an islet-like function of cells within these cultures. Note that little insulin or C-peptide is produced in the base medium that contains no DPFs.

[00081] **Example 11.** Both the quantity of insulin and the quantity of DNA were measured in IP cells subjected to differentiation culture with or without enzymatic detachment and subculturing. Cultures were carried out precisely as described in the previous paragraph. DNA was measured utilizing a standard Picogreen assay (Molecular Probes), while insulin was measured by ELISA assay. Total ng of Insulin was divided by total  $\mu$ g of DNA in the sample, thus providing the insulin:DNA ratio value, in order to calculate a ratio of the quantity of insulin present vs. the number of cells present (reflected by DNA content). The results are shown in Figure 14. In each of the differentiation media combinations, the insulin:DNA ratio is increased compared to base medium, suggesting that more insulin is produced on a per cell basis in the presence of DPFs than when cultured without them. Furthermore, the insulin:DNA ratio is increased slightly in some conditions upon glucose challenge (22mM glucose vs. 5mM), suggesting that the cells respond to glucose by releasing a greater quantity of insulin.

[00082] **Example 12.** Insulin-producing cells obtained by the preceding method were subjected to gene expression analysis as described above. Table 5 contains a list of the highest expressed genes, their position on the Clontech atlas 8K gene array, and relative expression of these genes (after normalization). Table 5 is attached hereto as Appendix 1

[00083] **Example 13.** Primary human pancreatic cells were seeded at  $0.5 \times 10^5$  cells/cm<sup>2</sup> in PCM on a collagen-1 surface and grown for 7 days. Insulin was measured at Days 1, 7, and 10 as follows: Growth medium was removed, wells were washed 3x in phosphate buffered saline. After a pre-incubation for 1 hour at 37C in base medium without insulin, with 5mM glucose, media was removed and replaced with either 1) base medium (without insulin) with 5mM glucose, or 2) base medium (without insulin) with 22mM glucose. Insulin was measured in cell-conditioned media after 18 hours at 37° C. After 7 days of culture, PCM medium was replaced with either 1) fresh PCM, 2) serum-free base medium, 3) serum free base medium with all 23 differentiating factors, 4) serum-free combination 1, or 5) serum-free combination 2. The results are shown in Figure 15. After 3 days exposure to the differentiating factors, increased insulin release is noted in presence of differentiating factors. The results on Day 1 argue against the

presence of a significant number of insulin-producing cells in the starting material, demonstrating the *de novo* generation of insulin-producing cells from acinar cells in the primary culture. It can be seen in the Figure that at the end of 10 days, insulin release in response to a glucose challenge is much greater in the DFP media than in the PCM or base medium, verifying the stimulatory effect that the DFPs exert on transformation of glandular epithelial cells into insulin-producing cells.

[00084] **Example 14.** Human pancreatic acinar cells were cultured on a collagen I surface in PCM from Day 1 to Day 7, thus generating a culture of IP cells at Day 7. On Day 7, the IP cells were washed and the PCM medium was replaced with the G09 differentiation medium containing the 30 factors listed in Table 2. At each time point (Days 1, 7, 10 and 14), insulin release was measured by washing the cultures three times with PBS, then challenging the cultures with a 1:1 mixture of DMEM and HAMs F12 containing either 5mM or 22mM glucose. After 18 hours of exposure to the glucose, supernatants were collected and insulin measured by ELISA. The results are shown in Figure 15a.

**III. Expression studies at several time points of primary human acinar cells that are expanded, allowed to differentiate into IP cells and then allowed to differentiate further into insulin-producing cells**

[00085] **Example 15.** Three independent samples of primary human pancreatic acinar cells were seeded and expanded described above. From Day 0 to Day 8, cells were on collagen I surface, seeded at  $10^4$  cells/cm<sup>2</sup>, in PCM. On Day 8, the medium was changed from PCM to the medium with the active factors shown in Table 2. Cells were fed twice with G09 (50% of medium replaced) between days 8 and 16. The cells remained on the surface throughout the culture process. Cultures were harvested at 3 days after the initial plating (actively trans-differentiating acinar cells), 8 days after plating (IP cells) and 16 days after plating (putative insulin producing cells) and subjected to gene expression analysis, as described in Example 7. mRNA expression data were obtained with 12K microarrays from Clonetech.

[00086] Briefly, growth medium was removed from the culture flasks and cells were lysed in trizol LS (Invitrogen) chaotrope/phenol reagent for about 2 minutes by pipetting the lysis solution over the cell layer. Three ml of RNase free water was added per 9 ml of lysis solution in an Oak Ridge Cetrifuge tube. 2.4 ml chloroform was then added and the solution vigorously vortexed for 1 minute. The aqueous and organic phases were then separated by cetrifugation at 4°C and the upper aqueous phase containing RNA was removed to a clean PET tube. The RNA was precipitated by isopropanol precipitation, washed with 70% ethanol and redissolved in 200 µl of RNase free water. A chaotrope lysis reagent was immediately added to the RNA and it was further purified using a Qiagen spin column method with a DNase digestion step. The purified RNA was finally eluted in 80µl RNase free water and stored at -80°C.

[00087] Labelled P-33 cDNA probes were prepared from the 30 µg of total RNA from each sample by first enriching for poly A + RNA using a streptavidin-magnetic bead separation method that is part of the Atlas Pure Total RNA Labeeling system. The labeled probes from each sample were hybridized with the plastic human 12 K gene arrays for about 16 hours, the arrays were washed and imaged according to the Atlas array protocols. The Atlas image 2.7 software was used to alignn array images with the array grid template and to exclude false background signals or false signals due to strong signal bleedover. The transcript signals were then extracted from these aligned arrays using the Atlas Image 2.7 software and further statistical analysis of the changes in gene expression were performed.

[00088] The raw expression data were analyzed as follows: (1) We filtered out genes that were not expressed at any of the 3 conditions/time points; (2) We normalized all of the microarrays against each other to remove differences from array-to-array and the effects of variability in sample processing, hybridization, etc.; (3) We identified genes which showed a statistically significant difference among the conditions/time points; and (4) We clustered the genes based on their temporal patterns in a way that is consistent with the design of the study and the changes in phenotype.

[00089] Table 6 shows expression data for the genes that were identified by the above analysis. This Table is attached hereto as Appendix 2. These identified genes were expressed at high levels at both Day 3 and Day 8, or their expression increased substantially between Day 3 and Day 8. The Table also shows the expression levels of these genes at Day 16, and the mean expression for all three condition/time points. The Table also shows the ratios of expression at various times: "I to A" is the ratio of expression of putative insulin-producing cells (Day 16) to acinar (Day 8) cells; "Int to A" is the ratio of IP cells (Day 8) cells to acinar cells (Day 3).

[00090] The data shown in Table 6 were further analyzed by clustering them into one of 17 "classes," whose features are summarized on the Table. A graphical representation of the characteristics of these 17 classes is presented in Figure 16.

[00091] The data from the Day 8 time points in Table 6 were also grouped with regard to whether the genes expressed at Day 8 in these cells belong to the classes of genes expressed normally in (1) liver and pancreas; (2) pancreas-associated genes; (3) liver-associated genes; or (4) progenitor-associated genes. The results are shown in Table 7.

**Table 7**

Genes Expressed In Liver and Pancreas	BDT Intermediate Cells			Hepatic Pattern of Expression			Pancreatic Pattern of Expression	
	Sample 1	Sample 2	Sample 3					
CK18	+	+	+	hepatic lineage			acinar cells	
CK8	+	+	+	hepatic lineage			acinar cells	
CK19	+	+	+	bile duct			duct cells	
CK7	+	+	+	bile duct			duct cells	
HNF1	+	+	+	liver tc factor			in beta cells	
$\alpha$ -1 antitrypsin	++	++	++	produced in differentiated hepatocytes			yes	
Notch-1	-	-	Trace	involved in differentiation of cells into hepatic lineage			developing pancreatic epithelium	
$\alpha$ -fetoprotein	-	-	-	developing hepatocytes and hepatic progenitors			developing pancreatic ducts	
Notch-3	Trace	Trace	Trace	Involved in differentiation of cells into hepatic lineage			pancreatic mesenchyme and endothelium	
Notch-4	Trace	Trace	Trace	involved in differentiation of cells into hepatic lineage			pancreatic mesenchyme and endothelium	
Jagged-2	+	+	+	involved in differentiation of cells into hepatic lineage			yes	
pi-glutathione s transferase (pi-GST)	+	+	++	developing liver			duct cells and centroacinar cells	
$\gamma$ -glutamyl transferase	-	-	-	developing bile duct			acinar cells	
Pancreas-Associated Genes								
	Sample 1	Sample 2	Sample 3	Hepatic Pattern of Expression			Pancreatic Pattern of Expression	
carbonic anhydrase	-	-	Trace				duct cells	
CF transmemb conductance regulator	-	-	Trace				duct cells	
elastase	-	-	-				acinar cells	
amylase	-	-	-				acinar cells	
insulin	+	Trace	Trace				islet	
somatostatin	Trace	Trace	Trace				islet	
Pancreatic Polypeptide	+	+	Trace				islet	
Glucagon	-	-	-				islet	

Liver-Associated Genes	Sample 1	Sample 2	Sample 3	Hepatic Pattern of Expression	Pancreatic Pattern of Expression
Sialyltransferase-6	-	-	-	- produced in differentiated hepatocytes	no
Liver-specific bHLH transcript factor	+	+	+	+ liver-specific Tc factor	no
Thy-1	+	+	+	+ hepatic oval cell marker	no
Glucose-6-phosphatase	-	-	Trace	hepatic lineage, progenitors and adult	No
Glutamine synthetase	-	-	Trace	hepatocyte	No
Carbamoyl phosphate synthetase-1	-	-	-	hepatocyte	no
Dipeptidylpeptidase IV	-	-	-	hepatocyte	no
C/EBP- $\alpha$	++	++	+	+ liver-specific Tc factor	*turned on and upregulated during hepatalization of pancreas (copper-deficient diet)
C/EBP-beta	++	++	++	+ liver-specific Tc factor	*turned on and upregulated during hepatalization of pancreas (copper-deficient diet)

Progenitor Cell-Associated Genes	Sample 1	Sample 2	Sample 3	Tissue
Musashi-1	-	-	-	Intestine
Nestin	-	-	-	Pancreas / Neuronal
CD34	-	-	-	Hematopoietic
Thy-1	-	-	-	Hepatic progenitors
BMP-2	-	-	-	Neuronal
BMPR $\alpha$ A	-	-	Trace	Mesenchyme
c-kit	-	-	-	Liver / Pancreas / Neuronal
chromogranin A	Trace	Trace	Trace	Neuroendocrine / Liver / Intestine
PDX-1	-	-	+	Pancreas

[00092] As can be seen, at Day 8 IP cells no longer expressed genes consistent with pancreatic acinar cells, nor did they express a complement of genes specific for pancreatic ductular cells. The IP cells expressed low levels of some markers associated with pancreatic islets, including insulin, somatostatin and pancreatic polypeptide, suggesting that at least some cells in the population are competent to express endocrine genes of the pancreatic islets.

[00093] Surprisingly, the IP cells also expressed several liver-specific transcription factors (*e.g.*, C/EBP alpha, C-EBP-beta) and other markers of mature and developing liver, including low levels of Thy-1, a marker associated with hepatic “oval” stem cells. This suggests that the differentiating cells were not moving simply from pancreatic acinar to pancreatic ductal, but had developed into a cell with both hepatic and pancreatic characteristics, while not fitting into any single gene expression profile of one of these cell types. The cells generated in this example resemble the cells that emerge from the pancreas of rodents that are fed a copper-deficient diet. (See, *e.g.* Rao et al., 1988). The pancreas of such animals goes through an acute phase of pancreatitis followed by “hepatization” of liver (which means cells that begin to express hepatic genes rather than pancreatic genes). Liver-like cells have also been reported in human fetal pancreas (Tsanadis et al., 1995) Isolated cells generated by the methods of the present invention (*e.g.*, by propagating primary acinar cells or other types of endodermal cells or progenitor cells by the methods of the invention) are to be distinguished from naturally occurring cells that may have some of the characteristics of IP cells, such as oval cells or cells isolated from the pancreas of a rodent on a copper-deficient diet.

[00094] Cells having the characteristics of these IP cells may be useful for, *e.g.*, therapeutic approaches in the treatment of diabetes. Furthermore, although the cells in this example were derived from pancreas, other epithelial tissues, or perhaps even any endoderm-derived tissue, may provide additional sources of cells that can be differentiated into cells having a similar phenotype. Suitable tissue types include, *e.g.*, liver or intestine. These IP cells express genes associated with pancreas, liver, intestine and neuronal tissues. For example, they express mucin, CK19 and CK7, which are

common markers associated with duct cells in the pancreas, liver and intestine. Thus, the gene expression pattern seen in these IP cells may serve as a predictive measure for cells derived from each of these tissues for the purpose of generating insulin-producing cells. Furthermore, IP cells may, under appropriate conditions, give rise, not only to pancreatic islet cells, but also to hepatocytes or any endoderm-derived tissue.

[00095] The disclosures of the following references, cited above in part, relate to the present invention:

WO 02/29010 A2 (Kerr-Conte);

Bonner-Weir, S. et al., Proc. Natl. Acad. Sci. USA 97: 7999-8004 (2000),

Bouwens, L., Microsc. Res. Tech. 43: 332-6 (1998);

Bowens, L. et al. Diabetologia 41:629-33 (1998);

Gmyr, V. et al., Diabetes 49:1671-80 (2000);

Gmyr, V. et al. Cell Transplant 10:109-21 (2001),

Gmyr, V. et al. Diabetes 49:1671-80 (2000),

Hall, P.A. et al., J. Pathol. 166: 97-103 (1992);

Kerr-Conte, J. et al., Diabetes 45:1108-14 (1996);

Kerr-Conte, J. et al., Transplant Proc 27:3268 (1985);

Pattou F. et al., Bull. Acad. Natl. Med. 184:1887-99 (2000);

Rao, MS et al Biochem Biophys Res Comm. 156:131-6 (1988);

Rooman, Ilse et al., Diabetes 51: 686-90 (2002);

Rooman, I. et al. Diabetologia 43:907-14 (2000);

Rooman, I. et al., Gastroenterology 121: 940-9 (2001);

Trivedi, N. et al. Endocrinology 142:2115-22 (2001);

Tsanadis, G. et al. Histol. Histopathol. 10:1-10 (1995);

Wang, R.N. et al., Diabetologia 38:1405-11(1995);

USP 6,011,647 (Ammon Peck).

[00096] The embodiments illustrated and discussed in the present specification are intended only to teach those skilled in the art the best way known to the inventors to make and use the invention, and should not be considered as limiting the scope of the

present invention. The exemplified embodiments of the invention may be modified or varied, and elements added or omitted, without departing from the invention, as appreciated by those skilled in the art in light of the above teachings. It is therefore to be understood that, within the scope of the claims and their equivalents, the invention may be practiced otherwise than as specifically described.

[00097] The entire disclosure of all applications, patents and publications, cited above and in the figures are hereby incorporated in their entirety by reference.

GENE	Position on Atlas 8K Array	Relative Expression, Sample 1	Relative Expression, Sample 2
aquaporin 5	7547	4539	4550
actin, beta	3952	3598	3442
actin, beta	8176	3047	3747
growth hormone secretagogue receptor	6846	2092	1710
profilin 1	448	1580	1246
special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold- associating DNAs)	3035	1437	886
cardiac-specific homeo box	2050	1395	2850
CCAAT/enhancer binding protein (C/EBP), beta	1588	1374	1671
RAS guanyl releasing protein 2 (calcium and DAG-regulated)	8262	1263	1616
cartilage paired-class homeoprotein 1	6677	1166	1241
paired-like homeodomain transcription factor 1	6805	1113	756
transcription factor 21	7621	1063	801
CD3E antigen, epsilon polypeptide (TTT3 complex)	8054	994	1113
CD151 antigen	5613	935	808
ATPase, Ca++ transporting, plasma membrane 2	7940	919	876
ficolin (collagen/fibrinogen domain- containing) 3 (Hakata antigen)	824	901	829
inositol polyphosphate phosphatase-like 1	5989	832	425
protein tyrosine phosphatase, receptor type, S	8367	806	810
integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VI <sub>A</sub> -3 receptor)	1743	758	647
syntaxis 1A (brain)	6851	743	658
parathymosin	7135	725	852
thymosin, beta 10	7436	709	1617
midkine (neurite growth-promoting factor 2)	2470	682	802
aryl/sulfatase A	3147	678	3084

calbindin 2, (29kD, calretinin)	7000	676
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	5214	668
retinal G protein coupled receptor myosin regulatory light chain 2, smooth muscle isoform	7972	653
butyrate response factor 1 (EGF-response factor 1)	2499	638
type I transmembrane receptor (seizure-related protein)	7325	630
type I transmembrane receptor (seizure-related protein)	7583	589
procollagen C-endopeptidase enhancer	3593	589
mitogen-activating protein kinase kinase kinase 2	7069	558
protease, serine, 1 (trypsin 1)	6323	558
pancreatitis-associated protein	4576	536
angiotensin receptor 1B	4093	516
stratifin	6489	503
keratin 17	7903	500
somatostatin receptor 3	6872	432
myosin-binding protein H	4692	428
ephrin-A5	4202	411
RAP1, GTPase activating protein 1	1965	407
chymotrypsinogen B1	6604	405
ankyrin-like with transmembrane domains 1	3577	395
Misshephen/NIK-related kinase	2439	391
bone morphogenetic protein 6	4492	381
splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated)	713	375
claudin 12	2720	370
matrix metalloproteinase 23A	7491	368
neurogranin (protein kinase C substrate, RC3)	4465	366
		335
		335

dopamine receptor D2	1649	362	234
cardiotrophin 1	5283	359	507
CCAAT/enhancer binding protein (C/EBP), alpha	7237	359	645
paired box gene 9	5206	335	201
protein tyrosine phosphatase, receptor type, N	8235	331	250
keratin 8	7215	327	449
claudin 7	280	325	173
trophinin associated protein (tastin)	462	323	360
neuronal thread protein	8356	322	366
basic helix-loop-helix domain containing, class B, 2	6734	318	215
annexin A2	4467	290	226
cathepsin D (lysosomal aspartyl protease)	7370	289	600
Bicaudal D ( <i>Drosophila</i> ) homolog 1	6822	284	217
lectin, galactoside-binding, soluble, 1 (galectin 1)	7331	280	310
keratin 7	7171	278	481
glyceraldehyde-3-phosphate dehydrogenase	3953	278	307
aquaporin 6, kidney specific	7591	277	258
TNF receptor-associated factor 1	6037	269	270
Rho GDP dissociation Inhibitor (GDI) alpha	5565	267	321
calcium channel, voltage-dependent, gamma subunit 4	3142	260	207
glutamate receptor, ionotropic, kainate 1 CCR4-NOT transcription complex, subunit 4	4776	244	296
filamin A, alpha (actin-binding protein-280)	983	244	428
peanut ( <i>Drosophila</i> )-like 1	3457	241	233
enhancer of rudimentary ( <i>Drosophila</i> ) homolog	711	233	310
endothelin converting enzyme 1	5921	231	405
	7835	229	197

rotocadherin 17	2483	223
quaporin 8	7679	217
ynapsin 1	4871	216
ubulin, alpha, brain-specific	2827	212
:D44 antigen (homing function and Indian blood group system)	7848	207
:erebral cavernous malformations 1	2731	205
:sulin-like 3 (Leydig cell)	666	202
:denylate cyclase activating polypeptide 1	4489	200
pituitary		36
:airless (mouse) homolog	5185	196
:sulin	4427	190
:ranulin	928	184
:early growth response 1	2111	184
:yclin-dependent kinase inhibitor 1A (p21, Cip1)	7852	178
:tem cell growth factor; lymphocyte secreted C-type lectin	1606	174
:CD4 antigen (p55)	5608	172
:CTAIRE protein kinase 1	6334	161
:Rho GTPase activating protein 6	1035	160
:3 protein-coupled receptor 37 (endothelin receptor type B-like)	6318	158
:syndecan 4 (amphiglycan, ryudocan)	3154	157
:CTAIRE protein kinase 3	8050	155
:empty spiracles (Drosophila) homolog 2	2084	150
:transglutaminase 1 (K polypeptide)	6674	150
:epidermal type I, protein-glutamine-gamma-glutamyltransferase)		101
:potassium voltage-gated channel, subfamily G, member 2	1335	147
:aldehyde dehydrogenase 4 (glutamate gamma-semialdehyde dehydrogenase; pyrroline-5-carboxylate dehydrogenase)	5985	147
:E1A binding protein p300	1433	144
		197

LIM homeobox transcription factor 1, beta	8211	143	89
eukaryotic translation elongation factor 2	4536	134	150
mitogen-activated protein kinase kinase	5462	129	92
Kinase 10			
PPAR(gamma) angiopoietin related protein	3074	129	56
homeo box A5	7037	128	87
CD63 antigen (melanoma 1 antigen)	7769	124	91
nuclear receptor coactivator 3	4181	119	84
CD68 antigen	443	118	256
transmembrane 4 superfamily member 7	1571	117	29
pancreatic polypeptide	2735	116	136
endothelin type b receptor-like protein 2	6656	114	74
neurogenin 1	5772	113	91
insulin receptor substrate 2	6016	110	130
glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	4702	109	58
neurotrophin 5 (neurotrophin 4/5)	8259	108	89
pyrimidinergic receptor P2Y, G-protein coupled, 6	3857	105	65
empty spiracles ( <i>Drosophila</i> ) homolog 1	2040	103	87
chromobox homolog 2 ( <i>Drosophila</i> Pc class)	2832	101	139
heart and neural crest derivatives expressed 1	2146	92	129
transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	7731	92	74
enolase 1, (alpha)	1389	92	205
thyroid transcription factor 1	4519	89	60
keratin 19	5923	88	223
Deleted in split-hand/split-foot 1 region	3641	87	104
glutathione peroxidase 4 (phospholipid hydroperoxidase)	1874	84	72
aristaless ( <i>Drosophila</i> ) homeobox	1783	81	103

GATA-binding protein 4	659	80	110
transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1), albumin proximal factor	712	80	136
heat shock transcription factor 1			
liver-specific bHLH-Zip transcription factor	6708	79	57
liver-specific bHLH-Zip transcription factor	765	77	188
eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD)	765	77	188
eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD)	6280	76	94
gamma-aminobutyric acid (GABA) A receptor, alpha 6	6280	76	94
retinoic acid receptor, gamma	5191	70	109
homeo box D9	1776	69	34
MAD1 (mitotic arrest deficient, yeast, homolog)-like 1	1946	63	38
homeo box A4	7177	57	103
Thy-1 cell surface antigen	559	57	87
talin	603	53	84
bone morphogenetic protein receptor, type II (serine/threonine kinase)	332	53	45
hepatocyte nuclear factor 3, alpha	72	52	60
Danodine receptor 2 (cardiac)	5244	47	40
signal transducer and activator of transcription 6, interleukin-4 induced	3661	40	35

APPENDIX 2: Table 6

SwissProt	Spot	geneName	day3	day6	day16	allMean	ratioItoA	relationItoA	classID	className
P04270	E19ab2	actin; alpha; cardiac muscle	1198.174	760	5955.077	2637.675	2.31E+00	-6.57E-01	7	Equal A/Int; Up Islets
O95996	N17ab2	adenomatous polyposis coli like	2708.542	5180	7594.139	5161.464	1.49E+00	9.36E-01	7	Equal A/Int; Up Islets
Q146597	G02ef0	alpha glucosidase II alpha subunit	306.0691	350	775.3358	477.0123	1.34E+00	1.92E-01	7	Equal A/Int; Up Islets
P14209	G23ab7	antigen identified by monoclonal	389.822	507	1238.43	711.8924	1.67E+00	3.80E-01	7	Equal A/Int; Up Islets
P30530	G14ef5	AXL receptor tyrosine kinase	314.4639	288	634.5658	412.2115	1.01E+00	-1.29E-01	7	Equal A/Int; Up Islets
O43770	I23ab3	B-cell CLL/lymphoma 7C	700.573	1050	1504.52	1065.931	1.10E+00	5.87E-01	7	Equal A/Int; Up Islets
O43852	P08ab3	calumenin	801.582	1290	4720.807	2269.921	2.56E+00	6.84E-01	7	Equal A/Int; Up Islets
O75718	O24cd6	cartilage associated protein	430.4432	256	1090.59	692.2327	1.34E+00	-7.52E-01	7	Equal A/Int; Up Islets
Q9Y3C0	G14ef4	CGI-116 protein	181.0293	301	416.7246	299.7237	1.20E+00	7.36E-01	7	Equal A/Int; Up Islets
P78369	G09cd6	claudin 10	1176.087	742	2598.595	1505.471	1.14E+00	-6.65E-01	7	Equal A/Int; Up Islets
P08572	P08ef4	collagen; type IV; alpha 2	1130.23	1350	4684.425	2389.488	2.05E+00	2.60E-01	7	Equal A/Int; Up Islets
P11802	B05ef5	cyclin-dependent kinase 4	914.1579	978	2342.994	1411.839	1.36E+00	9.79E-02	7	Equal A/Int; Up Islets
Q16555	O07ab4	dihydropyrimidinase-like 2	114.6165	164	921.1473	399.8267	3.01E+00	5.14E-01	7	Equal A/Int; Up Islets
P33316	H23ab2	dUTP pyrophosphatase	177.2032	238	541.5382	318.7836	1.61E+00	4.23E-01	7	Equal A/Int; Up Islets
P07992	K20ef6	excision repair cross-complement	362.031	415	907.933	561.6388	1.33E+00	1.97E-01	7	Equal A/Int; Up Islets
O75636	B14cd3	ficolin (collagen/fibrinogen domain)	1081.127	1010	4327.606	2139.448	2.00E+00	-9.87E-02	7	Equal A/Int; Up Islets
Q9UBA6	B19ef4	G6 protein	370.6842	578	1489.206	812.6378	2.01E+00	6.41E-01	7	Equal A/Int; Up Islets
Q9V5P5	P08ef7	GDP-mannose pyrophosphoryl	171.1216	198	414.0862	261.0679	1.27E+00	2.10E-01	7	Equal A/Int; Up Islets
O75293	E02ef7	growth arrest and DNA-damage-1	194.3626	203	388.6833	281.3841	9.92E-01	6.35E-02	7	Equal A/Int; Up Islets
P50152	C05ab6	guanine nucleotide binding protein	204.743	150	497.3097	283.8702	1.28E+00	-4.53E-01	7	Equal A/Int; Up Islets
Q9N9X09	C05gh3	HIF-1 responsive RTP801	348.8574	253	1032.929	545.0622	1.57E+00	-4.61E-01	7	Equal A/Int; Up Islets
P05204	J22ab7	high-mobility group (nonhistone) c	2067.865	1120	6059.895	3082.818	1.55E+00	-8.84E-01	7	Equal A/Int; Up Islets
Q9P0P2	C17ef3	homolog of yeast MOG1	325.8407	378	682.7568	452.1583	1.07E+00	2.14E-01	7	Equal A/Int; Up Islets
Q9NWF8	L15gh2	hypothetical protein FLJ10055	172.167	241	374.3	262.6222	1.12E+00	4.88E-01	7	Equal A/Int; Up Islets
Q9NWV4	B17gh2	hypothetical protein FLJ20580	221.4432	280	483.5381	328.2481	1.13E+00	3.37E-01	7	Equal A/Int; Up Islets
Q9PS8	A21ef3	hypothetical protein HSPC195	153.824	165	330.9111	216.4274	1.11E+00	9.72E-02	7	Equal A/Int; Up Islets
Q9BWS8	P04gh5	hypothetical protein MGC3234	196.9154	161	427.2066	261.7132	1.12E+00	-2.90E-01	7	Equal A/Int; Up Islets
Q9BSK0	K21gh3	hypothetical protein MGC4415	156.4692	117	684.3425	319.1224	2.13E+00	-4.25E-01	7	Equal A/Int; Up Islets
Q9YGM1	P09cd6	IGF-II mRNA-binding protein 2	135.2566	153	408.5101	232.2937	1.59E+00	1.79E-01	7	Equal A/Int; Up Islets
Q9NQX7	H10gh2	integral membrane protein 3	478.2728	481	1102.244	687.2575	2.00E+00	8.97E-03	7	Equal A/Int; Up Islets
P08648	E23ef7	integrin; alpha 5 (fibronectin rec)	183.4629	124	478.7265	262.0713	1.38E+00	-5.65E-01	7	Equal A/Int; Up Islets
O00410	J24ab6	karyopherin (importin) beta 3	326.6874	196	629.7655	384.2402	9.47E-01	-7.35E-01	7	Equal A/Int; Up Islets
P07195	N16ab6	lactate dehydrogenase B	1003.971	1200	5593.079	2595.05	2.48E+00	2.57E-01	7	Equal A/Int; Up Islets
P09382	N22ab6	lectin; galactoside-binding; solub	19170.52	35400	78085.75	4205.77	2.03E+00	8.83E-01	7	Equal A/Int; Up Islets
O75427	P20ab6	leucine-rich repeat protein; neur	174.5605	231	543.3883	316.5457	1.63E+00	4.03E-01	7	Equal A/Int; Up Islets
Q16553	A15ab7	lymphocyte antigen 6 complex Ic	425.8933	494	938.4504	619.3701	1.14E+00	2.13E-01	7	Equal A/Int; Up Islets
O75900	O05cd4	matrix metalloproteinase 23A	381.2184	297	851.7221	510.1038	1.16E+00	-3.58E-01	7	Equal A/Int; Up Islets
Q9UNF1	H16ef7	melanoma antigen; family D; 2	193.8125	219	659.9701	357.6132	1.77E+00	1.77E-01	7	Equal A/Int; Up Islets
P13995	J16cd6	methylene tetrahydrofolate dehy	321.4876	226	759.6021	435.6746	1.24E+00	-5.09E-01	7	Equal A/Int; Up Islets
O00265	G19cd8	microtubule-associated protein; f	189.7616	234	377.5576	267.156	9.93E-01	3.03E-01	7	Equal A/Int; Up Islets
P27361	B13ef5	mitogen-activated protein kinase	358.0872	382	720.3119	486.849	1.01E+00	9.38E-02	7	Equal A/Int; Up Islets
P24844	E18cd5	myosin; light polypeptide 5; regul	5480.451	7380	22518.95	11793.05	2.04E+00	4.29E-01	7	Equal A/Int; Up Islets
Q9NVD4	J10gh2	N-acetylneuraminc acid phosph	153.762	167	390.6642	237.1908	1.35E+00	1.26E-01	7	Equal A/Int; Up Islets
Q9Y617	N22ef8	phosphoserine aminotransferase	169.9503	250	1238.851	553.0005	2.87E+00	5.58E-01	7	Equal A/Int; Up Islets
O95356	A11gh7	pituitary tumor-transforming 3	237.2126	192	276.181	901.8229	3.26E+00	-3.05E-01	7	Equal A/Int; Up Islets
Q9Y5X6	G04cd6	plasma glutamate carboxypeptid	169.6268	142	366.6202	226.0168	1.11E+00	-2.58E-01	7	Equal A/Int; Up Islets
Q15113	G20ab8	procollagen C-endopeptidase en	497.3967	402	2628.947	1176.046	2.40E+00	-3.08E-01	7	Equal A/Int; Up Islets
O15460	D20cd4	procollagen-proline; 2-oxoglutar	262.1395	433	758.4003	483.9569	1.53E+00	7.25E-01	7	Equal A/Int; Up Islets
O43556	I19gh1	sarcoglycan; epsilon	172.7191	215	349.304	245.5263	1.02E+00	3.13E-01	7	Equal A/Int; Up Islets
P50454	M17ab6	serine (or cysteine) proteinase In	339.1762	612	4091.161	1680.942	3.59E+00	8.53E-01	7	Equal A/Int; Up Islets
Q92853	A23cd8	similar to vaccinia virus HindIII K	444.062	553	997.4551	684.6951	1.17E+00	3.15E-01	7	Equal A/Int; Up Islets
Q16658	P20cd1	singed-like (fascin homolog); sea	262.7872	479	1472.155	738.014	2.49E+00	8.66E-01	7	Equal A/Int; Up Islets
P09478	E18cd7	Sm protein F	257.2026	278	548.9705	351.3772	1.09E+00	1.12E-01	7	Equal A/Int; Up Islets
Q9BVH9	D18gh7	thioredoxin related protein	522.062	481	1903.964	986.9954	1.87E+00	-1.18E-01	7	Equal A/Int; Up Islets
Q9HB0	L08gh8	Thy-1 co-transcribed	327.3502	374	1110.527	603.8101	1.76E+00	1.90E-01	7	Equal A/Int; Up Islets
P01033	P09ef7	tissue inhibitor of metalloproteinase	1236.457	1500	13029.41	5256.661	3.40E+00	2.83E-01	7	Equal A/Int; Up Islets
Q15582	L20ef6	transforming growth factor; beta-1	1221.063	2060	8540.86	3939.09	2.61E+00	7.51E-01	7	Equal A/Int; Up Islets
Q01995	M07cd2	transgelin	3307.821	3880	18534.27	8573.074	2.49E+00	2.29E-01	7	Equal A/Int; Up Islets
Q13641	B05ab2	trophoblast glycoprotein	479.6488	426	1399.786	768.6158	1.55E+00	-1.70E-01	7	Equal A/Int; Up Islets
P06468	G08cd2	tryptophanyl 2 (beta)	339.2292	589	13203.05	4710.469	5.28E+00	7.96E-01	7	Equal A/Int; Up Islets
P51784	M21cd4	ubiquitin specific protease 11	158.0478	194	491.1248	280.9819	1.64E+00	2.94E-01	7	Equal A/Int; Up Islets
P03996	E17ab2	actin; alpha 2; smooth muscle; al	412.1137	1940	4180.134	1471.763	6.66E+00	2.23E+00	9	Increasing A/Int/I
P06123	P02ef6	collagen; type I; alpha 2	186.5566	576	14565.36	5109.251	6.29E+00	1.63E+00	9	Increasing A/Int/I
P24821	A05ef7	hexabration (tenascin C; cyto	355.495	918	2371.983	1215.165	2.74E+00	1.37E+00	9	Increasing A/Int/I
Q9NV42	F13gh3	hypothetical protein FLJ10849	374.1495	861	3471.789	1568.848	3.21E+00	1.20E+00	9	Increasing A/Int/I
P40261	M09cd1	nicotinamide N-methyltransferas	1060.579	2310	5683.533	3016.993	2.42E+00	1.12E+00	9	Increasing A/Int/I
Q15063	C01ef7	osteoblast specific factor 2 (fasc	276.6334	795	8328.222	3133.301	4.91E+00	1.52E+00	9	Increasing A/Int/I
P09486	A09ef7	secreted protein; acidic; cysteine	404.2839	2760	6383.72	2233.48	7.30E+00	2.77E+00	9	Increasing A/Int/I
P35625	K20ef5	tissue inhibitor of metalloproteinase	216.254	619	10078.17	3637.823	5.54E+00	1.52E+00	9	Increasing A/Int/I
Q9H2L5	G06gh8	AD037 protein	361.2297	681	158.8121	400.4602	-1.19E+00	9.15E-01	19	Intr>(A;I)
P15121	C18ab2	aldo-keto reductase family 1; me	2342.744	5380	2337.052	3354.494	-3.51E-03	1.20E+00	19	Intr>(A;I)
P08582	B14ef5	antigen p97 (melanoma associat	299.1375	595	80.80392	324.9781	-1.89E+00	9.92E-01	19	Intr>(A;I)
P20292	E05ab2	arachidonate 5-lipoxygenase-act	100.0016	687	203.2911	330.0345	1.02E+00	2.78E+00	19	Intr>(A;I)
O15342	A13ab3	ATPase; H <sup>+</sup> transporting; lysoso	6063.171	16500	6160.831	9572.914	2.31E-02	1.44E+00	19	Intr>(A;I)
Q9BXJ0	H18gh6	C1q and tumor necrosis factor re	180.2978	350	154.1441	228.0109	-2.26E-01	9.55E-01	19	Intr>(A;I)
Q9NRJ3	P09gh4	CC chemokine CCL28	250.0021	1830	763.2666	948.0274	1.61E+00	2.87E+00	19	Intr>(A;I)
P05305	F17ab5	endothelin 1	866.4561	1810	403.431	1026.992	-1.10E+00	1.06E+00	19	Intr>(A;I)
P09341	A04ab6	GRO1 oncogene (melanoma gro	933.2938	4770	1006.711	2236.622	1.09E-01	2.35E+00	19	Intr>(A;I)
Q9Z730	O14ef5	GTP-binding protein	653.8575	2760	542.7528	1318.381	-2.69E-01	2.08E+00	19	Intr>(A;I)
Q9H5K0	L10gh5	hypothetical protein FLJ23360	151.2029	296	130.3196	192.6442	-2.14E-01	9.71E-01	19	Intr>(A;I)
O19554	E21ef7	integrand; beta 6	540.0342	1180	233.0555	650.9277	-1.21E+00	1.13E+00	19	Intr>(A;I)

P42701	A06ef7	Interleukin 12 receptor; beta 1	1227.347	22100	1333.521	8218.994	1.20E+01	4.17E+00	19	Inl> (A;I)
P09237	J15ef1	matrix metalloproteinase 7 (matril	9598.545	87300	19849.69	38905.32	1.05E+00	3.18E+00	19	Inl> (A;I)
P16860	O13ab8	natriuretic peptide precursor B	4340.214	12900	1260.906	6171.6	-1.78E+00	1.57E+00	19	Inl> (A;I)
P21359	L16ab7	neurofibromat 1 (neurofibromato	132.483	292	155.0822	183.3208	2.27E+01	1.14E+00	19	Inl> (A;I)
P02775	B07ef7	pro-platelet basic protein (includ	33.98656	1400	265.2119	567.1992	2.96E+00	5.37E+00	19	Inl> (A;I)
Q9UDQ9	J22gh4	SBB126 protein	121.5886	1080	238.8624	479.5908	9.74E-01	3.15E+00	19	Inl> (A;I)
Q75635	P14cd3	serine (or cysteine) proteinase In	232.6336	3890	326.2581	1483.169	4.88E-01	4.06E+00	19	Inl> (A;I)
P02735	A11cd3	serum amyloid A1	496.9578	17400	957.6141	6295.724	9.46E-01	5.13E+00	19	Inl> (A;I)
O60635	F10cd5	tetraspan 1	321.8888	843	177.8479	447.5729	-8.58E-01	1.39E+00	19	Inl> (A;I)
P50591	C05cd4	tumor necrosis factor (ligand) su	536.7773	1550	476.2305	854.3061	-1.73E-01	1.53E+00	19	Inl> (A;I)
Q03169	I10ef7	tumor necrosis factor; alpha-Indu	366.7502	1260	326.6536	650.583	-1.56E-01	1.78E+00	19	Inl> (A;I)
Q9C075	N11ef8	type I Intermediate filament cyto	848.9829	4200	401.4854	1818.182	-1.08E+00	2.31E+00	19	Inl> (A;I)
P02248	A01cd3	ubiquitin C	155.6735	892	62.04595	369.9913	-1.33E+00	2.52E+00	19	Inl> (A;I)
Q95497	A15cd5	vann 1	309.1556	1840	510.7208	887.0948	7.24E+01	2.57E+00	19	Inl> (A;I)
Q14202	B15cd5	zinc finger protein 261	199.6246	1040	247.9161	496.3668	3.13E-01	2.38E+00	19	Inl> (A;I)
P15514	M02ef7	amphiregulin (schwannoma-derm	103.1419	405	65.66067	191.2981	-8.52E-01	1.97E+00	18	Off A/I; On Int
Q9BZL9	I21gh8	B aggressive lymphoma gene	126.3951	211	84.56927	140.8098	-5.80E-01	7.42E-01	18	Off A/I; On Int
P30991	D14ef5	chemokine (C-X-C motif); recept	64.37115	260	120.2328	148.3131	9.01E-01	2.02E+00	18	Off A/I; On Int
P29400	H13ab3	collagen; type IV; alpha 5 (Alp)	53.50943	374	141.1609	189.6904	1.40E+00	2.81E+00	18	Off A/I; On Int
Q9UJ22	H22cd7	F-box only protein 2	87.59822	217	120.3781	141.4646	4.59E-01	1.31E+00	18	Off A/I; On Int
Q16769	O15cd8	glutaminyl-peptidase cyclotransfe	89.90252	195	113.0683	132.7502	3.31E-01	1.12E+00	18	Off A/I; On Int
P02261	M06gh8	H2A histone family; member 1	65.46028	263	126.664	151.868	9.52E-01	2.01E+00	18	Off A/I; On Int
P20769	D03ef1	immunoglobulin heavy constant r	101.245	176	102.5687	126.7136	1.87E-02	8.00E-01	18	Off A/I; On Int
P52945	I12ab6	insulin promoter factor 1; homeo	74.60504	351	86.42558	170.7555	1.21E-01	2.24E+00	18	Off A/I; On Int
Q14496	F21cd6	interferon-induced protein 44	99.27101	266	98.28057	161.3017	-1.45E-01	1.53E+00	18	Off A/I; On Int
P01583	F15ef7	Interleukin 1; alpha	103.386	375	66.6314	181.5566	-6.34E-01	1.86E+00	18	Off A/I; On Int
P01584	F17ef7	Interleukin 1; beta	116.7675	415	119.0156	216.8707	2.75E-02	1.83E+00	18	Off A/I; On Int
Q9GZM1	I20gh7	NDRG family member 4	102.1328	348	101.569	183.8736	-7.99E-03	1.77E+00	18	Off A/I; On Int
P25105	G15ef5	platelet-activating factor receptor	97.43121	356	80.47935	177.9689	-2.76E-01	1.87E+00	18	Off A/I; On Int
P58294	O14gh8	prokinin 1 precursor	79.98268	241	137.5167	152.9437	7.82E-01	1.59E+00	18	Off A/I; On Int
P23471	A06ef6	protein tyrosine phosphatase; re	85.55935	346	93.65845	175.0253	1.30E-01	2.02E+00	18	Off A/I; On Int
O88386	D10ef3	RAB10; member RAS oncogene	123.2003	399	68.13944	196.7342	-8.54E-01	1.69E+00	18	Off A/I; On Int
P10826	I08gh6	retinoid acid receptor; beta	67.98871	241	120.9469	143.3844	8.31E-01	1.83E+00	18	Off A/I; On Int
O95786	I24ef3	RNA helicase	112.9366	241	89.32396	147.8829	-3.38E-01	1.10E+00	18	Off A/I; On Int
P02778	O10ef7	small inducible cytokine subfamli	65.03395	418	86.09019	189.6022	4.05E-01	2.68E+00	18	Off A/I; On Int
P80162	F14cd1	small inducible cytokine subfamli	54.00821	311	129.2639	164.6594	1.26E+00	2.52E+00	18	Off A/I; On Int
P43005	N23ef5	solute carrier family 1 (neuronal/	99.30514	189	10.81119	133.1898	1.58E-01	9.32E-01	18	Off A/I; On Int
P01375	O09ef6	tumor necrosis factor (TNF super	138.6153	386	75.13436	200.0804	-8.84E-01	1.48E+00	18	Off A/I; On Int
Q16890	G04cd2	tumor protein D52-like 1	103.5477	191	98.01862	130.885	-7.92E-02	8.84E-01	18	Off A/I; On Int
Q9H949	K11gh5	WW45 protein	111.8812	218	79.54574	136.5769	-4.92E-01	9.64E-01	18	Off A/I; On Int
Q9H4G4	O06gh5	17kD fetal brain protein	88.61746	223	532.2979	281.2148	2.59E+00	1.33E+00	8	Off Adnar; Increasing Int/I
Q14040	B15ef1	collagen; type VI; alpha 1	38.27203	209	472.4143	165.1794	9.65E+00	2.45E+00	8	Off Adnar; Increasing Int/I
P12110	B17ef1	collagen; type VI; alpha 2	68.00282	164	383.637	136.2467	4.54E-01	8.97E-01	8	Off Adnar; Increasing Int/I
P02751	K15ef1	fibronectin 1	4.441362	152	417.1.603	1442.812	9.88E-05	5.10E+00	8	Off Adnar; Increasing Int/I
P14652	N23ab6	homeo box B2	62.71629	291	351.1974	1308.575	5.83E+00	2.21E+00	8	Off Adnar; Increasing Int/I
P08476	D15ef7	Inhibitor A (activin A; activin	64.38161	318	854.6532	412.2794	3.73E+00	2.30E+00	8	Off Adnar; Increasing Int/I
P17936	D07ab6	insulin-like growth factor binding	38.22268	349	1302.669	563.1937	5.09E+00	3.19E+00	8	Off Adnar; Increasing Int/I
Q9Y4K0	P18ab6	lysyl oxidase-like 2	75.91549	260	2525.644	953.7036	5.06E+00	1.77E+00	8	Off Adnar; Increasing Int/I
P03956	N05ef7	matrix metalloproteinase 1 (Inte	106.2193	203	590.2622	299.8442	2.47E+00	9.35E-01	8	Off Adnar; Increasing Int/I
P39900	N15ef7	matrix metalloproteinase 12 (mac	18.2367	381	121.9553	539.7471	6.06E+00	4.39E+00	8	Off Adnar; Increasing Int/I
P55001	G09ab7	microfibrillar-associated protein 2	99.33548	526	3302.631	1309.293	5.06E+00	2.40E+00	8	Off Adnar; Increasing Int/I
Q9NYR0	O07gh7	SH3-domain kinase binding prot	34.69271	197	656.4675	261.0285	4.24E+00	2.50E+00	8	Off Adnar; Increasing Int/I
O43623	D06ef4	small homolog 2 ( <i>Drosophila</i> )	96.88079	292	3028.508	1139.155	4.97E+00	1.59E+00	8	Off Adnar; Increasing Int/I
P09936	I13cd4	ubiquitin carboxy-terminal ester	48.30052	219	1523.166	596.7714	4.98E+00	2.18E+00	8	Off Adnar; Increasing Int/I
Q02952	J11ab2	A kinase (PRKA) anchor protein	103.9756	364	229.1446	232.3779	1.14E+00	1.81E+00	4	Off Adnar; On Int=I
Q99541	I19ab2	adipose differentiation-related pr	67.38509	182	146.1347	132.005	1.12E+00	1.44E+00	4	Off Adnar; On Int=I
P54284	N17ab3	calcium channel; voltage-dependen	106.3248	227	254.95633	195.965	1.26E+00	1.09E+00	4	Off Adnar; On Int=I
Q12629	G14ab5	cAMP responsive element bindin	100.66369	193	217.7521	170.529	1.11E+00	9.40E-01	4	Off Adnar; On Int=I
Q9NPF2	M02ef4	chondroitin 4-sulfotransferase	133.8375	192	303.01	209.7612	1.18E+00	5.24E-01	4	Off Adnar; On Int=I
Q9H7A5	F12gh7	chromosome 20 open reading fra	98.71521	179	208.0134	161.8637	1.08E+00	8.58E-01	4	Off Adnar; On Int=I
Q9H9Q2	L23gh5	COP9 constitutive photomorpho	86.57682	115	184.3088	128.7341	1.09E+00	4.14E-01	4	Off Adnar; On Int=I
P42771	D17ef5	cyclin-dependent kinase inhibitor	43.35217	471	355.7426	290.1928	3.04E+00	3.44E+00	4	Off Adnar; On Int=I
Q14650	J20ef4	cytoplasmic FMR1 interacting pr	132.5759	272	321.6348	242.2271	1.28E+00	1.04E+00	4	Off Adnar; On Int=I
Q96IK6	F14gh6	DKFZP434C245 protein	145.227	104	91.06477	113.265	-6.73E-01	4.89E-01	4	Off Adnar; On Int=I
P12034	D05ef7	fibroblast growth factor 5	60.2377	259	317.6018	212.2747	2.40E+00	2.10E+00	4	Off Adnar; On Int=I
Q93079	M20gh6	H2B histone family; member J	144.6906	428	271.2983	281.3281	9.07E-01	1.56E+00	4	Off Adnar; On Int=I
Q9P016	A10ef8	HSPC144 protein	123.4601	348	399.4935	290.4476	1.69E+00	1.50E+00	4	Off Adnar; On Int=I
Q9HB15	M09gh4	HT021	116.3605	276	309.5798	233.8335	1.41E+00	1.24E+00	4	Off Adnar; On Int=I
Q9BY45	O24gh8	HTPAP protein	78.49388	109	177.2043	121.5622	1.17E+00	4.74E-01	4	Off Adnar; On Int=I
P08397	G18ab6	hydroxymethylblane synthase	139.0857	188	260.8417	195.1361	9.07E-01	4.38E-01	4	Off Adnar; On Int=I
Q9BUV0	M06gh4	hypothetical protein dJ465N24.2.	68.40543	152	167.5592	129.3473	1.29E+00	1.15E+00	4	Off Adnar; On Int=I
Q9H9A2	N22gh6	hypothetical protein DKFZp762L	82.54725	110	169.5379	120.7311	1.04E+00	4.16E-01	4	Off Adnar; On Int=I
Q9NUV6	P09gh3	hypothetical protein FLJ11113	87.43713	178	136.6771	134.1021	6.44E-01	1.03E+00	4	Off Adnar; On Int=I
Q9NXF7	C20gh2	hypothetical protein FLJ20280	66.49705	143	170.7367	126.7851	1.36E+00	1.11E+00	4	Off Adnar; On Int=I
Q9H6V0	M05gh5	hypothetical protein FLJ21839	116.3704	258	323.3964	232.5844	1.47E+00	1.15E+00	4	Off Adnar; On Int=I
Q9BW5	K21gh6	hypothetical protein M3G4707	80.31127	170	203.9516	151.3887	1.34E+00	1.08E+00	4	Off Adnar; On Int=I
Q9H765	I15gh6	hypothetical protein MGCG540	106.3949	220	206.6405	177.6046	9.58E-01	1.05E+00	4	Off Adnar; On Int=I
Q14157	N23gh1	KIAA0144 gene product	95.13957	147	147.7214	129.9305	6.35E-01	6.27E-01	4	Off Adnar; On Int=I
Q9Y2D8	A07ef8	KIAA0923 protein	84.1225	237	206.8269	176.1358	1.30E+00	1.50E+00	4	Off Adnar; On Int=I
Q9H6Z3	E24gh5	kinesin family member 13A	111.6382	206	238.6822	185.578	1.10E+00	8.85E-01	4	Off Adnar; On Int=I
Q99748	J24ab8	neurturin	123.7488	150	246.4754	173.2957	9.94E-01	2.74E-01	4	Off Adnar; On Int=I
Q9IVD7	D11gh3	parvlin; alpha	82.67948	140	230.66	151.1753	1.48E+00	7.62E-01	4	Off Adnar; On Int=I
Q42175	W24gh6	rhomboid-like protease domain	98.R1458	110	107.7372	125.6164	1.11E+00	1.11E+00	4	Off Adnar; On Int=I

Q13636	K19cd7	RAB31; member RAS oncogene	76.36263	118	170.0352	121.5169	1.15E+00	6.30E-01	4 Off Adnar; On Int=
Q9UIC2	L10ef2	RNB6	80.76879	171	194.395	148.7422	1.27E+00	1.08E+00	4 Off Adnar; On Int=
Q9NVQ7	K12gh3	Sed61 alpha form 2	82.6036	143	162.0674	129.1434	9.72E-01	7.89E-01	4 Off Adnar; On Int=
Q75368	J08cd1	SH3 domain binding glutamic acid	92.82513	212	196.8753	167.1823	1.08E+00	1.19E+00	4 Off Adnar; On Int=
Q95863	N01cd2	small homolog 1 (Drosophila)	76.58448	134	157.9807	122.817	1.04E+00	8.06E-01	4 Off Adnar; On Int=
Q9UL01	H01cd8	squamous cell carcinoma antigen	86.70353	111	176.4557	124.5829	1.03E+00	3.51E-01	4 Off Adnar; On Int=
Q16226	N05cd6	thioredoxin Interacting protein	111.1384	454	529.2322	364.6675	2.25E+00	2.03E+00	4 Off Adnar; On Int=
P07996	A11ef7	thrombospondin 1	79.00174	139	163.2593	127.0819	1.05E+00	8.15E-01	4 Off Adnar; On Int=
Q99081	F10ef6	transcription factor 12 (HTF4; he	112.2294	181	256.0348	182.9347	1.19E+00	6.86E-01	4 Off Adnar; On Int=
Q95922	L06ef7	tubulin tyrosine ligase-like 1	73.12945	245	253.9213	190.8311	1.80E+00	1.75E+00	4 Off Adnar; On Int=
P15036	H18ef6	vels erythroblastosis virus E26 c	149.9259	114	83.55955	115.8531	-8.43E-01	-3.94E-01	4 Off Adnar; On Int=
Q95337	D04ef8	weakly similar to glutathione per	69.55111	164	284.3593	172.7489	2.03E+00	1.24E+00	4 Off Adnar; On Int=
Q9H185	M18gh5	xylosyltransferase II	81.87715	106	174.2539	120.5878	1.09E+00	3.68E-01	4 Off Adnar; On Int=
P55263	K07ab2	adenosine kinase	891.6698	720	299.6337	637.198	-1.57E+00	-3.08E-01	15 On A/Int; Down
P51648	A22ab2	aldehyde dehydrogenase 3 family	1955.203	1390	507.3785	1284.046	-1.95E+00	-4.93E-01	15 On A/Int; Down
P50995	I08ab2	annexin A11	4888.71	3870	1773.94	3511.843	-1.46E+00	-3.36E-01	15 On A/Int; Down
P12429	H14ab2	annexin A3	9711.235	10800	1720.452	7424.351	-2.50E+00	1.59E-01	15 On A/Int; Down
P05026	L22ab2	ATPase; Na+/K+ transporting; be	3965.733	5290	1976.367	3744.962	-1.00E+00	4.16E-01	15 On A/Int; Down
P00751	M07ab3	B-factor; proprdin	2984.309	2460	1178.473	2206.568	-1.34E+00	-2.81E-01	15 On A/Int; Down
Q9HA23	E10gh6	calponin like transmembrane dom	480.5263	528	193.0456	400.5912	-1.32E+00	1.36E-01	15 On A/Int; Down
Q16170	M17ab3	carcinoembryonic antigen-related	984.7628	1236	212.7712	807.5766	-2.21E+00	3.15E-01	15 On A/Int; Down
P25774	P07ab5	cathepsin S	857.9751	776	228.9093	620.9386	-1.91E+00	-1.45E-01	15 On A/Int; Down
P21926	J13ef7	CD9 antigen (p24)	2011.966	3500	833.332	2115.74	-1.27E+00	8.00E-01	15 On A/Int; Down
Q9H247	M18gh5	chemokine (C-X-C motif) ligand 1	650.7961	842	235.8205	576.1228	-1.46E+00	3.71E-01	15 On A/Int; Down
O14493	G21ab4	claudin 4	1919.128	2480	799.5104	1732.749	-1.26E+00	3.70E-01	15 On A/Int; Down
P12277	M06ab4	creatinine kinase; brain	373.8119	617	193.0681	394.4895	-9.53E-01	7.22E-01	15 On A/Int; Down
Q9NY57	E20ef4	CS box-containing WD protein	596.6891	384	211.1821	397.3278	-1.50E+00	-6.35E-01	15 On A/Int; Down
P53355	D09ab5	death-associated protein kinase	1325.243	1260	558.9756	1048.818	-1.25E+00	-7.03E-02	15 On A/Int; Down
O15205	D17cd6	diubiquitin	7363.301	14700	2196.358	8102.423	-1.75E+00	1.00E+00	15 On A/Int; Down
Q9UF22	C23ef8	DKFZP564K247 protein	1325.797	1060	313.5237	900.9109	-2.08E+00	-3.18E-01	15 On A/Int; Down
P28562	M22ab5	dual specificity phosphatase 1	2077.188	1680	754.9876	1502.884	-1.46E+00	-3.09E-01	15 On A/Int; Down
Q16690	B21ab4	dual specificity phosphatase 5	485.6475	305	155.0161	315.2743	-1.65E+00	-6.70E-01	15 On A/Int; Down
Q9UJW0	H10ef1	dynactin 4 (p62)	778.5079	662	335.9831	592.1023	-1.21E+00	-2.34E-01	15 On A/Int; Down
E13gh5		endonuclease pyrophosphatase	233.9728	378	183.3797	265.0097	-3.52E-01	6.91E-01	15 On A/Int; Down
P00533	A06ef5	epidermal growth factor receptor	263.2516	334	182.4044	259.7582	-5.29E-01	3.42E-01	15 On A/Int; Down
Q13113	J02cd5	epithelial protein up-regulated in	13324.19	15500	2641.961	10494.6	-2.33E+00	2.20E+01	15 On A/Int; Down
P28161	M09ab6	glutathione S-transferase M2 (m	1020.341	690	217.4433	642.7437	-2.23E+00	-5.63E-01	15 On A/Int; Down
Q03013	L06ab3	glutathione S-transferase M4	333.2767	465	210.8696	336.4683	-6.60E-01	4.81E-01	15 On A/Int; Down
P52594	A18ab4	HIV-1 Rev binding protein	439.4544	468	252.8058	386.6697	-7.98E-01	9.00E-02	15 On A/Int; Down
Q9NWT9	D05gh2	hypothetical protein FLJ20607	1062.388	757	368.3558	729.2943	-1.53E+00	-4.89E-01	15 On A/Int; Down
Q9BZ4R	L12gh7	hypothetical protein HT036	748.0681	844	160.1449	584.0643	-2.22E+00	1.74E-01	15 On A/Int; Down
Q9BW25	A19gh6	hypothetical protein MGC3101	315.4695	409	150.4768	291.8079	-1.07E+00	3.76E-01	15 On A/Int; Down
P16144	H16ab6	integrin; beta 4	490.7243	672	157.31	440.0464	-1.64E+00	4.54E-01	15 On A/Int; Down
P10145	O22ef7	interleukin 6	6902.735	13300	1783.339	7330.866	-1.85E+00	9.47E-01	15 On A/Int; Down
Q05084	G10ab7	islet cell autoantigen 1 (69kD)	600.5671	588	209.1328	465.8994	-1.52E+00	-3.05E-02	15 On A/Int; Down
Q9Y484	E14cd7	JM5 protein	1335.218	2010	938.9827	1429.625	-5.08E-01	5.93E-01	15 On A/Int; Down
P14923	M23ef6	junction plakoglobin	1969.949	2610	912.3081	1831.613	-1.11E+00	4.07E-01	15 On A/Int; Down
P05763	N06ef6	keratin 18	17317.24	12500	2306.177	10707.79	-2.91E+00	-4.70E-01	15 On A/Int; Down
P08727	L06ab5	keratin 19	4025.258	2800	631.8404	2484.93	-2.67E+00	-5.25E-01	15 On A/Int; Down
P08729	N14ef6	keratin 7	11605.48	11100	1886.88	8203.912	-2.62E+00	-6.19E-02	15 On A/Int; Down
P05787	N16ef6	keratin 8	11031.01	7880	1694.024	6867.677	-2.70E+00	9.47E-01	15 On A/Int; Down
O14782	H22ab2	kinesin family member 3C	366.3528	652	242.2822	420.177	-5.97E-01	8.31E-01	15 On A/Int; Down
O00515	D05ab7	ladinin 1	3562.632	2040	824.2377	2140.683	-2.11E+00	-8.08E-01	15 On A/Int; Down
P80188	D13ab7	lipocalin 2 (oncogene 24p3)	5234.435	9070	664.0466	4989.308	-2.98E+00	7.93E-01	15 On A/Int; Down
Q9UQ53	G02ef3	mannosyl (alpha-1;3)-glycoprote	1485.546	931	398.5069	938.2331	-1.90E+00	-6.75E-01	15 On A/Int; Down
P80294	D15gh6	metallothionein 1H	327.8489	366	208.8705	300.7815	-6.50E-01	1.57E-01	15 On A/Int; Down
Q75394	M10cd5	mitochondrial ribosomal protein L	411.6574	646	213.7295	433.794	-1.05E+00	5.49E-01	15 On A/Int; Down
Q9Y376	H18ef2	MD25 protein	860.3225	1410	550.0258	939.6431	-6.45E-01	7.11E-01	15 On A/Int; Down
P15941	H22ab7	mucin 1; transmembrane	2330.649	1250	487.1995	1357.116	-2.25E+00	-8.95E-01	15 On A/Int; Down
Q16301	H11cd1	myelin transcription factor 2	2433.02	2560	545.0513	1844.855	-2.16E+00	7.14E-02	15 On A/Int; Down
Q99836	M07ab7	myeloid differentiation primary re	1088.39	1110	413.4864	871.4196	-1.40E+00	3.15E-02	15 On A/Int; Down
P24001	H08cd4	natural killer cell transcript 4	49232.84	71300	1351.68	44684.13	-1.86E+00	5.34E-01	15 On A/Int; Down
Q9SC002	O12gh8	normal mucosa of esophagus sp:	8605.554	17700	4423.686	10242.28	-9.60E-01	1.04E+00	15 On A/Int; Down
P25963	A16ef6	nuclear factor of kappa light pol	938.908	1270	605.6118	937.0159	-6.33E-01	4.32E-01	15 On A/Int; Down
P00491	L18ab7	nucleoside phosphorylase	820.4015	500	250.4586	523.7383	-1.71E+00	-7.13E-01	15 On A/Int; Down
P49763	O20ef7	placental growth factor; vascular	5604.053	12600	1723.953	6646.258	-1.70E+00	1.17E+00	15 On A/Int; Down
Q9Y342	A13ef2	plasmidpin	942.5595	983	300.2833	742.036	-1.65E+00	6.10E-02	15 On A/Int; Down
P43490	H04cd5	pre-B-cell colony-enhancing fact	2261.27	1730	651.3251	1546.408	-1.80E+00	-3.90E-01	15 On A/Int; Down
Q99988	B23ef7	prostate differentiation factor	1470.061	2930	681.8854	1694.613	-1.11E+00	9.96E-01	15 On A/Int; Down
Q9UJY1	B05ef3	protein kinase H11	1836.927	2080	544.441	1485.828	-1.75E+00	1.77E-01	15 On A/Int; Down
Q9H1C7	O10gh8	putative nuclear protein ORF1-Fl	11454.74	14800	3062.014	9771.26	-1.90E+00	3.69E-01	15 On A/Int; Down
P51149	A21ef6	RAB7; member RAS oncogene f	3422.13	5250	2267.107	3646.784	-5.94E-01	6.18E-01	15 On A/Int; Down
P51151	J22cd4	RAB9A; member RAS oncogene	1882.687	1580	721.6194	1393.904	-1.38E+00	-2.55E-01	15 On A/Int; Down
P15153	C17ef6	ras-related C3 botulinum toxin st	383.0769	418	213.0301	338.0922	-8.47E-01	1.26E-01	15 On A/Int; Down
P52566	H19ef1	Rho GDP dissociation inhibitor (	986.1501	788	352.0789	708.6827	-1.49E+00	-3.24E-01	15 On A/Int; Down
P01011	I08ef7	serine (or cysteine) proteinase In	40450.89	43700	10172.44	31439.89	-1.99E+00	1.11E-01	15 On A/Int; Down
P05120	P07ef7	serine (or cysteine) proteinase In	24922.82	38200	2879.818	21999.69	-3.11E+00	6.16E-01	15 On A/Int; Down
O14508	M13ef6	STAT induced STAT Inhibitor-2	1511.844	1490	420.453	1139.68	-1.85E+00	-2.42E-02	15 On A/Int; Down
Q9Y6N5	G13gh4	sulfide dehydrogenase like (yeas	823.7665	871	284.0637	659.5107	-1.54E+00	7.99E-02	15 On A/Int; Down
O00161	C23cd4	synaptosomal-associated protein	1077.833	1340	687.0432	1034.031	-6.50E-01	3.11E-01	15 On A/Int; Down
P31431	F24cd1	syndecan 4 (amphiglycan; ryno)	2109.871	3080	887.6687	2026.067	-1.25E+00	5.46E-01	15 On A/Int; Down
O15533	B16ef7	TAP binding protein (lapasin)	313.1585	424	162.2501	299.8834	-9.48E-01	4.38E-01	15 On A/Int; Down
P17497	F11ef5	T-complex 1	405.6787	298	157.6175	317.0491	-1.65E+00	-7.35E-01	15 On A/Int; Down

Q16149	B15cd1	transporter 1; ATP-binding cassette	862.1561	1100	480.86685	813.3307	-8.42E-01	3.47E-01	15 On A/int; Down
Q9Y2A9	C22ef3	UDP-GlcNAc beta-1,3-N	774.5506	436	153.9485	454.8446	-2.33E+00	-8.29E-01	15 On A/int; Down
O60625	N10cd3	vesicle-associated membrane protein	2480.8688	2680	584.39	1914.133	-2.09E+00	1.10E-01	15 On A/int; Down
P07948	A21ab7	v-yes-1 Yamaguchi sarcoma virus	512.646	443	170.1742	375.1466	-1.59E+00	-2.12E-01	15 On A/int; Down
Q9P2N4	M10gh4	a disintegrin-like and metalloproteinase	159.7274	227	72.96867	153.1495	-1.13E+00	5.06E-01	14 On A/int; Dif
P47895	C04ab2	aldehyde dehydrogenase 1 family	1247.008	2370	146.6644	1254.954	-3.09E+00	9.27E-01	14 On A/int; Dif
P04233	G09ef1	CD74 antigen (invariant polypept)	229.4566	174	86.99566	163.6002	-1.40E+00	-3.96E-01	14 On A/int; Off
Q9N231	L12gh4	chromosome 20 open reading frame	345.4771	375	137.4415	285.9642	-1.33E+00	1.18E-01	14 On A/int; Off
O96002	G07cd5	chromosome X open reading frame	401.521	375	130.7318	302.4558	-1.62E+00	-9.81E-02	14 On A/int; Dif
O94907	J15gh6	dickkopf homolog 1 (Xenopus lat)	150.3215	200	84.53571	145.044	-8.30E+00	4.14E-01	14 On A/int; Dif
Q92796	K06ef5	discs; large (Drosophila) homolog	161.9581	154	84.80819	133.5184	-9.32E-01	-7.56E-02	14 On A/int; Off
Q13115	O17ab4	dual specificity phosphatase 4	533.5415	730	146.312	469.8392	-1.87E+00	4.52E-01	14 On A/int; Off
P29317	F02ef5	EphA2	267.722	279	82.15254	209.5143	-1.70E+00	5.78E-02	14 On A/int; Off
P29323	D10ef5	EphB2	269.1596	232	74.35016	191.9946	-1.86E+00	-2.11E-01	14 On A/int; Off
Q9Ukf9	H10cd7	ets homologous factor	603.0262	587	102.0333	430.6372	-2.56E+00	-3.92E-02	14 On A/int; Off
Q9NP03	P22gh2	exosome component Rrp41	273.527	309	49.72784	207.9117	-2.46E+00	1.36E-01	14 On A/int; Off
O43524	G12ab4	forkhead box O3A	262.2734	169	102.6453	177.9385	-1.35E+00	-6.35E-01	14 On A/int; Off
P21217	M16ab3	fucosyltransferase 3 (galactosidase)	189.3354	257	60.24803	168.8097	-1.65E+00	4.40E-01	14 On A/int; Off
O75205	D24ef2	G protein-coupled receptor; family	621.7284	382	90.93956	364.8596	-2.77E+00	-7.03E-01	14 On A/int; Off
O75712	A03ef1	gap junction protein; beta 3; 31kDa	253.3139	402	145.54566	260.8655	-6.93E-01	7.72E-01	14 On A/int; Off
Q92908	D12ab4	GATA binding protein 6	293.117	199	93.59788	195.3976	-1.65E+00	-5.55E-01	14 On A/int; Off
O95210	P05cd4	genethonin 1	331.9855	241	112.69	228.6851	-1.56E+00	-4.60E-01	14 On A/int; Off
O95395	K21cd5	glucosaminyl (N-acetyl) transferase	297.4236	274	45.82301	205.5863	-2.70E+00	-1.21E-01	14 On A/int; Off
P48506	F22ab5	glutamate-cysteine ligase; catalytic	299.1944	243	134.9982	225.879	-1.15E+00	-2.97E-01	14 On A/int; Off
Q9U198	F08ef8	hqp256 protein	357.587	336	106.803	266.8154	-1.74E+00	-8.96E-02	14 On A/int; Off
Q9H6D8	D18gh5	hypothetical protein FLJ22362	542.6184	595	127.4299	421.5312	-2.09E+00	1.32E-01	14 On A/int; Off
P05362	I02ab6	intercellular adhesion molecule 1	411.0131	424	67.80016	301.0074	-2.60E+00	4.56E-02	14 On A/int; Off
Q07627	J20gh7	keratin associated protein 1.1	288.3566	303	40.28571	210.3957	-2.84E+00	6.93E-02	14 On A/int; Off
Q9BYQ7	D10gh8	keratin associated protein 4.10	493.4934	605	96.51137	398.2261	-2.35E+00	2.93E-01	14 On A/int; Off
O75071	F15gh1	KIAA0494 gene product	240.2512	167	91.77931	166.3595	-1.39E+00	-5.24E-01	14 On A/int; Off
Q9UPC02	G22ef8	KIAA1100 protein	224.7248	349	135.6811	236.4102	-2.78E-01	6.34E-01	14 On A/int; Off
O43896	H10cd6	kinesin family member 1C	159.6982	170	73.49424	134.4385	-1.12E+00	9.16E-02	14 On A/int; Off
Q13887	L05ab5	Kruppel-like factor 5 (intestinal)	494.1259	376	97.43054	322.6178	-2.34E+00	-3.93E-01	14 On A/int; Off
O00312	D22cd3	MAP kinase-interacting serine/threonine	147.9629	150	66.60695	128.2701	-7.73E-01	2.20E-02	14 On A/int; Off
O15264	H07ab8	mitogen-activated protein kinase	213.7425	160	76.32069	150.0667	-1.49E+00	-4.17E-01	14 On A/int; Off
Q9UHA4	P10gh1	mitogen-activated protein kinase	268.8101	244	72.50042	195.0133	-1.89E+00	-1.41E-01	14 On A/int; Off
P21397	F23ef6	monoamine oxidase A	427.3495	480	30.42645	312.5207	-3.81E+00	1.67E-01	14 On A/int; Off
P55196	N07ab7	myeloid/lymphoid or mixed-lineage	164.9238	168	78.62952	137.1449	-1.07E+00	2.56E-02	14 On A/int; Off
Q12965	I24ab7	myosin IIE	212.4935	276	122.00015	203.3655	-8.01E-01	3.75E-01	14 On A/int; Off
Q9HBW1	O10gh7	NAG14 protein	417.9837	396	86.84398	300.2834	-2.27E+00	-7.79E-02	14 On A/int; Off
Q9H2W4	D20gh2	neural precursor cell expressed; 361.6431	361.6431	463	75.41197	299.9778	-2.26E+00	3.56E-01	14 On A/int; Off
Q9NR32	O06gh4	non-kinase Cdc42 effector protein	194.8075	327	117.0936	213.1256	-7.34E-01	7.49E-01	14 On A/int; Off
P23511	M19ab8	nuclear transcription factor Y; alpha	239.2485	226	132.3351	199.2783	-8.54E-01	-8.06E-02	14 On A/int; Off
Q9N650	D14cd4	oncosinatin M receptor	337.1614	233	141.0848	237.114	-1.26E+00	-5.33E-01	14 On A/int; Off
P04085	O16ef7	platelet-derived growth factor alpha	441.7554	453	124.4793	343.2015	-1.83E+00	6.89E-02	14 On A/int; Off
Q13048	N05cd2	pregnancy specific beta 1-glycoprotein	149.7737	203	84.53571	145.8869	-8.25E-01	4.41E-01	14 On A/int; Off
P10586	E11ef6	protein tyrosine phosphatase; regulatory	465.2876	405	136.6718	335.6682	-1.77E+00	-2.05E-01	14 On A/int; Off
O95200	N22ab8	retinoic acid receptor responder 1	237.2899	315	72.62858	275.0752	-2.59E+00	-4.72E-01	14 On A/int; Off
Q9NVX8	P17ef3	Rho GTPase activating protein 8	425.2848	479	109.2541	337.8544	-1.96E+00	1.72E-01	14 On A/int; Off
Q15418	M14ef5	ribosomal protein S6 kinase; 90kDa	299.5258	361	78.38666	246.2347	-1.93E+00	2.68E-01	14 On A/int; Off
Q15434	F10ab8	RNA binding motif; single strand	454.6438	328	145.2434	309.3377	-1.65E+00	-4.70E-01	14 On A/int; Off
Q15437	O10cd6	Sec23 homolog B (S. cerevisiae)	281.2005	235	126.9582	214.4633	-1.15E+00	-2.58E-01	14 On A/int; Off
O60679	D15ef5	serum-inducible kinase	202.0368	194	62.20916	152.8498	-1.70E+00	-5.63E-02	14 On A/int; Off
Q12890	N05ef5	SFRS protein kinase 1	350.4057	278	113.0428	247.1823	-1.63E+00	-3.33E-01	14 On A/int; Off
Q12971	L03cd6	sialyltransferase	247.3141	329	96.91022	234.3379	-1.35E+00	4.11E-01	14 On A/int; Off
P78556	M02cd2	small inducible cytokine subfamily	308.0437	382	59.31325	249.7105	-2.36E+00	3.10E-01	14 On A/int; Off
Q75751	F14ef4	solute carrier family 22 (extreme)	164.6419	238	66.83593	156.4431	-1.30E+00	5.31E-01	14 On A/int; Off
Q9UM01	D08cd8	solute carrier family 7 (caloric ai)	201.657	260	55.89528	172.4611	-1.85E+00	3.66E-01	14 On A/int; Off
Q9Y5X1	D10ef2	sortilin	219.1839	240	108.9101	189.2981	-1.01E+00	1.30E-01	14 On A/int; Off
P08842	D19ab3	steroid sulphatase (microsomal); a	436.4255	414	136.2997	328.904	-1.68E+00	-7.62E-02	14 On A/int; Off
O43760	G09cd5	synaptojanin 2	391.0545	238	118.1167	249.1866	-1.73E+00	-7.14E-01	14 On A/int; Off
O75674	N15cd5	target of myb-1 like 1 (chicken)	276.5234	285	54.32353	205.2456	-2.35E+00	4.30E-02	14 On A/int; Off
P01135	K04ef7	transforming growth factor; alpha	215.9023	160	59.63082	145.3108	-1.86E+00	-4.29E-01	14 On A/int; Off
Q9NT70	K13gh3	transmembrane protein vezatin	365.9385	401	129.2607	298.7991	-1.50E+00	1.33E-01	14 On A/int; Off
O60656	G13gh3	UDP glycosyltransferase 1 family	546.3937	438	27.51254	337.3961	-4.31E+00	-3.18E-01	14 On A/int; Off
Q9NZ42	N18gh4	uncharacterized hematopoietic st	196.9377	213	115.2737	175.1842	-7.73E-01	1.15E-01	14 On A/int; Off
Q76080	E14cd4	zinc finger protein 215	314.9706	211	74.56541	200.0768	-2.08E+00	-5.80E-01	14 On A/int; Off
Q13015	H11ab2	ALL1-fused gene from chromosome	329.6061	1730	1752.9	172.138	2.41E+00	2.40E+00	6 On Adchar; Up Int=1
P04083	I06ab3	annexin A1	1114.486	8240	8292.245	5883.787	2.90E+00	2.89E+00	6 On Adchar; Up Int=1
O60592	B14ab2	Arg/Abl-interacting protein ArgBP	1576.114	3320	2017.836	2304.427	3.56E-01	1.07E+00	6 On Adchar; Up Int=1
Q07814	E04ef5	BCL2-associated X protein	430.8903	862	110.1457	797.9572	1.35E+00	1.00E+00	6 On Adchar; Up Int=1
Q14201	E17cd7	BTG family; member 3	197.8608	451	419.4378	355.9496	1.08E+00	1.19E+00	6 On Adchar; Up Int=1
Q9NR00	J21gh4	chromosome 8 open reading frame	2766.931	7310	3283.111	4453.955	2.47E-01	1.40E+00	6 On Adchar; Up Int=1
Q9BUW7	K19gh6	chromosome 9 open reading frame	228.4878	650	551.4272	476.5934	1.27E+00	1.51E+00	6 On Adchar; Up Int=1
O95401	N04cd4	cofactor required for Sp1 transcript	186.3494	395	588.6133	390.063	1.66E+00	1.08E+00	6 On Adchar; Up Int=1
Q00535	B09ef5	cyclin-dependent kinase 5	269.7495	476	432.1176	392.629	6.80E-01	8.19E-01	6 On Adchar; Up Int=1
P21741	E17ab7	midkine (neurite growth-promotion)	2991.463	15400	9802.656	9388.855	1.71E+00	2.36E+00	6 On Adchar; Up Int=1
Q9Y291	J15ef2	mitochondrial ribosomal protein L	177.4689	330	365.4484	290.8529	1.04E+00	8.93E-01	6 On Adchar; Up Int=1
O75376	E17cd6	nuclear receptor co-repressor 1	375.3679	1270	727.3836	791.9381	9.54E-01	1.76E+00	6 On Adchar; Up Int=1
P03973	N10cd1	secretory leukocyte protease inhibitor	592.855	2070	4153.51	2270.718	2.81E+00	1.80E+00	6 On Adchar; Up Int=1
O15427	F06cd4	solute carrier family 16 (monocar-	228.58	753	785.8975	589.0175	1.78E+00	1.72E+00	6 On Adchar; Up Int=1
P16949	D11ab7	stathmin 1/oncoprotein 18	728.2643	2630	1984.807	1781.654	1.45E+00	1.85E+00	6 On Adchar; Up Int=1
Q9NZ86	J08gh3	uncharacterized bone marrow protein	311.3754	945	536.938	597.7198	7.86E-01	1.60E+00	6 On Adchar; Up Int=1

P50440	A09ab5	glycine amidinotransferase (L-arg)	1737.906	395	261.2318	798.1958	-2.73E+00	-2.14E+00	20 Other
P29622	A06cd1	serine (or cysteine) proteinase	In 461.3518	189	264.9574	304.9848	-8.00E-01	-1.29E+00	20 Other
O14646	C17eb4	chromodomain helicase DNA bln	867.7631	180	273.1703	440.3418	-1.57E+00	-2.27E+00	20 Other
P48307	I10cd4	lissue factor pathway inhibitor 2	920.3007	366	277.6619	521.385	-1.73E+00	-1.33E+00	20 Other
Q15125	D08cd6	enopamil binding protein (sterol)	897.4306	230	282.4317	470.0852	-1.67E+00	-1.96E+00	20 Other
P19387	B13ab8	polymerase (RNA) II (DNA direct)	196.4282	155	282.8549	211.5128	5.26E-01	-3.39E-01	20 Other
Q9P0K7	H08gh6	retinoic acid induced 14	177.983	275	283.8007	245.4643	6.73E-01	6.26E-01	20 Other
P30086	E04ab8	prostatic binding protein	634.2686	462	300.6211	465.627	-1.08E+00	-4.57E-01	20 Other
Q13045	C06ab5	flightless I homolog (Drosophila)	622.7072	501	306.0777	476.5407	-1.02E+00	-3.14E-01	20 Other
O95084	G10cd7	prolease; serine; 23	1096.7556	246	314.746	552.6166	-1.80E+00	-2.15E+00	20 Other
P49770	L11ef4	eukaryotic translation initiation fa	731.6826	547	329.7361	536.2071	-1.15E+00	-4.19E-01	20 Other
Q13948	J02ef5	cit-like 1; CCAAT displacement	1 222.2758	349	330.5149	300.5112	5.72E-01	6.50E-01	20 Other
Q32021	H05ab3	hemochromatosis	205.1607	291	339.4607	278.446	7.26E-01	5.03E-01	20 Other
PS2895	H16gh6	aldo-keto reductase family 1; me	4001.572	263	339.7988	1534.634	-3.56E+00	-3.93E+00	20 Other
Q9Y5N1	M24cd7	histamine receptor H3	526.5133	203	341.1301	356.7517	-6.26E-01	-1.38E+00	20 Other
P43378	N23ab3	protein tyrosine phosphatase; no	1360.729	445	368.4734	724.8175	-1.88E+00	-1.61E+00	20 Other
P55414	O11ab2	angiotensin receptor-like 1	620.7039	406	395.8948	474.2345	-6.49E-01	-6.12E-01	20 Other
Q14802	K03cd1	FXYD domain-containing ion trar	2174.215	711	402.87	1096.127	-2.43E+00	-1.61E+00	20 Other
Q9Y256	F16cd5	nuclear distribution gene C home	745.3985	447	408.3037	533.6945	-8.68E-01	-7.37E-01	20 Other
P30043	O21ab3	biliverdin reductase B (flavin redi	877.8813	565	417.1383	620.0433	-1.07E+00	-6.35E-01	20 Other
Q9NPT3	L06gh3	uncharacterized hematopoietic st	804.2103	448	421.5183	557.2055	-9.32E-01	-8.51E-01	20 Other
Q12972	D17ab8	protein phosphatase 1; regulator	251.1796	358	425.52	345.0523	7.61E-01	5.13E-01	20 Other
Q9Y256	N21ef2	PTD009 protein	738.5086	424	436.6114	532.9995	-7.58E-01	-8.01E-01	20 Other
Q02750	K02ef7	mitogen-activated protein kinase	810.206	508	441.4249	586.6635	-8.76E-01	-6.72E-01	20 Other
P42226	G23cd2	signal transducer and activator o	692.6025	516	450.4229	619.5565	-9.87E-01	-7.92E-01	20 Other
P31947	M07ef6	stratin	2941.197	741	452.267	1378.205	-2.70E+00	-1.95E+00	20 Other
P46597	J12ab2	acetylserotonin O-methyltransfer	2225.944	437	466.9229	1043.272	-2.25E+00	-2.35E+00	20 Other
O14745	J24cd4	solute carrier family 9 (sodium/hy	1844.719	642	504.4269	997.106	-1.87E+00	-1.52E+00	20 Other
Q9NS67	D24gh1	G protein-coupled receptor 27	1464.475	381	595.0192	813.4043	-1.30E+00	-1.94E+00	20 Other
Q9UKL5	J07cd8	programmed cell death 6 Interact	995.6375	886	605.9272	829.3129	-7.16E-01	-1.68E-01	20 Other
Q9UOL3	B11ef2	liver-specific bHLH-Zip transcript	825.7324	1150	606.7901	860.8974	-4.44E-01	4.78E-01	20 Other
Q9NZ21	P18ef2	hypothetical protein HSPC138	397.5554	450	618.4035	488.5944	6.37E-01	1.78E-01	20 Other
Q9Y3Q3	H03cd7	Integral type I protein	526.2023	355	631.4284	504.2124	2.63E-01	-5.68E-01	20 Other
Q9NSN3	C10gh4	similar to aspartate beta hydroxy	355.1305	273	667.4052	431.8528	9.10E-01	-3.79E-01	20 Other
Q9Y5Z0	B12cd7	beta-sitosterol APP-cleaving enzyme 2	1469.687	960	680.3343	1036.811	-1.11E+00	-6.14E-01	20 Other
C21gh7	C21gh7	H2B histone family; member B	511.589	855	733.4035	699.9713	5.20E-01	7.41E-01	20 Other
O14713	M11cd5	Integrin cytoplasmic domain-ass	446.3806	746	737.9643	643.5595	7.25E-01	7.42E-01	20 Other
P46095	P11ab4	G protein-coupled receptor 6	2336.841	460	760.4217	1185.918	-1.62E+00	-2.34E+00	20 Other
Q9BV10	K07gh6	hypothetical protein MGC3136	1761.627	653	779.7338	1064.815	-1.18E+00	-1.43E+00	20 Other
Q99653	O08cd7	calcium binding protein P22	1713.549	1430	793.2363	1313.03	-1.11E+00	-2.59E-01	20 Other
P41584	P16gh1	polymerase (RNA) II (DNA direct)	560.1066	892	821.9856	758.0427	5.53E-01	6.71E-01	20 Other
P11940	E06ab8	poly(A) binding protein; cytoplas	1738.585	669	827.8343	1078.525	-1.07E+00	-1.38E+00	20 Other
Q00341	G21ab6	high density lipoprotein binding p	545.5844	444	866.5328	618.5713	6.67E-01	2.99E-01	20 Other
Q15795	K08ab7	NADH dehydrogenase (ubiquinol)	1582.872	1199	873.0748	1214.409	-8.56E-01	-4.15E-01	20 Other
Q13082	E05ab7	microtubule-associated protein 4	1217.396	472	873.8683	854.4272	-4.78E-01	-1.37E+00	20 Other
P36405	D16ab2	ADP-ribosylation factor-like 3	508.3031	547	939.7284	665.1099	8.87E-01	1.07E-01	20 Other
Q9NKH2	C04gh2	hypothetical protein FLJ20254	515.6731	457	959.9781	647.4269	8.97E-01	-1.44E-01	20 Other
Q9Y323	D21ef2	hypothetical protein HSPC177	836.9663	1630	976.2242	1148.545	2.19E-01	9.59E-01	20 Other
P48059	H12ab7	LIM and senescent cell antigen-II	560.9674	918	1003.945	827.7691	8.40E-01	7.11E-01	20 Other
Q9POM8	M02ef2	mitochondrial ribosomal protein l	579.0083	836	1024.359	846.5801	8.23E-01	6.93E-01	20 Other
Q13813	E07cd2	spectrin; alpha; non-erythrocytic	2261.592	886	1070.984	1406.107	-1.08E+00	-1.35E+00	20 Other
Q9Y379	H07ef2	CGI-69 protein	2556.713	1900	1174.107	1877.939	-1.12E+00	-4.26E-01	20 Other
Q13247	O13gh1	splicing factor; arginine/serine-ri	718.1614	1210	1194.951	1041.827	7.35E-01	7.55E-01	20 Other
P14416	D03ef6	dopamine receptor D2	814.5351	745	1299.03	952.9439	6.73E-01	-1.28E-01	20 Other
Q06323	A15ef7	proteasome (prosome; macropain)	1491.803	2350	1386.719	1742.377	-1.05E-01	6.55E-01	20 Other
Q9NF31	H17gh4	SAR1 protein	752.6343	886	1386.849	1008.646	8.82E-01	2.36E-01	20 Other
P05451	C07cd3	regenerating Islet-derived 1 alpha	75644.12	1690	1394.425	26243.72	-5.76E+00	-5.48E+00	20 Other
P04075	C12ab2	aldolase A; fructose-bisphosphat	4534.199	1590	1470.967	2532.66	-1.62E+00	-1.51E+00	20 Other
Q15904	A19ab3	ATPase; H+ transporting lysoso	833.0193	1380	1471.793	1228.765	8.21E-01	7.30E-01	20 Other
P15559	G24ef7	NAD(P)H dehydrogenase; quinol	537.0892	303	1486.45	775.5735	1.47E-01	-8.25E-01	20 Other
Q00303	L20cd3	eukaryotic translation initiation fa	1243.805	636	1556.448	1145.377	3.23E-01	-9.68E-01	20 Other
P56705	M01gh7	wingless-type MMTV integration	3569.752	1590	1635.805	2271.364	-1.13E+00	-1.18E+00	20 Other
P39210	I04ef7	MpV17 transgene; murine homol-	990.336	894	1723.06	1202.587	7.99E-01	-1.47E-01	20 Other
Q9UKL9	N03ef4	aldo-keto reductase family 1; me	16311.31	2840	1896.102	7016.796	-3.10E+00	-2.52E+00	20 Other
Q43516	E12cd3	Wiskott-Aldrich syndrome protein	1162.511	1190	1979.246	1444.29	7.68E-01	3.51E-02	20 Other
Q9Y470	D01ef7	stem cell growth factor lymphoc	1346.693	1110	2049.542	1503.556	6.06E-01	-2.73E-01	20 Other
P29312	H12cd4	tyrosine 3-monooxygenase/trypt	5187.766	4710	2331.854	4076.247	-1.15E+00	-1.40E-01	20 Other
Q9Y5R8	P24gh4	MUM2 protein	1596.032	1750	2568.113	1971.095	6.86E-01	1.32E-01	20 Other
P17676	D01ab5	CCAAT/enhancer binding protel	6064.068	2880	2723.688	3890.676	-1.15E+00	-1.07E+00	20 Other
Q95362	F11gh6	differentially expressed in hemat	10407.52	2880	2912.158	5333.102	-1.84E+00	-1.96E+00	20 Other
O60417	C11gh7	S100 calcium binding protein A1	6955.642	5690	3097.579	5248.939	-1.17E+00	-2.89E-01	20 Other
P19623	E17cd2	spermidine synthase	1644.266	1020	3417.978	2027.643	1.06E+00	-6.88E-01	20 Other
Q9P039	P02ef7	FXYD domain-containing ion trar	2410.08	2120	4486.029	3004.627	8.96E-01	-1.87E-01	20 Other
Q9BUF5	F05gh8	tubulin beta-5	2252.623	1580	4730.755	2855.744	1.07E+00	-5.08E-01	20 Other
P00995	C23cd2	serine protease inhibitor; Kazal t	67989.21	11300	5416.175	28226.58	-3.65E+00	-2.59E+00	20 Other
P11142	E22ef7	heat shock 70kD protein 8	11154.99	7840	5433.843	8144.601	-1.04E+00	-5.08E-01	20 Other
P10620	E16ef7	microsomal glutathione S-transfe	6706.736	2430	5571.411	4901.595	-2.68E-01	-1.47E+00	20 Other
Q13347	N02cd3	eukaryotic translation initiation fa	19633.03	5210	5660.757	10168.91	-1.79E+00	-1.91E+00	20 Other
P15680	B16cd1	ribosomal protein S2	4356.01	2060	5964.993	4127.437	4.54E-01	-1.08E+00	20 Other
Q9HCU0	E24gh4	tumor endothelial marker 1 prec.	3139.145	2600	7148.075	4295.784	1.19E+00	-2.72E-01	20 Other
Q04941	O16ab5	proteolipid protein 2 (colonie epit	17951.73	11600	8567.736	12775.93	-1.07E+00	-6.04E-01	20 Other
Q9UP11	M14cd2	small nuclear ribonucleoprotein I	4625.515	8280	8998.787	7300.387	9.60E-01	8.39E-01	20 Other
P13987	B18ef7	CD59 antigen p18-20 (antigen Id	17383.17	19200	10453.43	15673.38	-7.34E-01	1.42E-01	20 Other

Q9UJ09	L02gh4	13kDa differentiation-associated	1754.698	1990	2889.148	2210.196	7.19E-01	1.79E-01	3 Unchanged High
Q9Y6H1	E23ef2	16.7kD protein	5687.333	4050	5837.94	5191.628	3.77E-02	4.90E-01	3 Unchanged High
Q9POU1	C07gh3	6.2 kD protein	2323.402	1990	3847.586	2721.439	7.28E-01	-2.21E-01	3 Unchanged High
P80095	N10ab7	6-pyruvoyl-tetrahydropterin synth	3223.922	2620	1569.69	2471.592	-1.04E+00	-2.99E-01	3 Unchanged High
Q92747	F04ab2	actin related protein 2/3 complex	4894.401	3990	3030.018	3972.89	-6.92E-01	-2.93E-01	3 Unchanged High
O15144	F08ab2	actin related protein 2/3 complex	13976.76	21400	17206.31	17538.09	3.00E-01	6.17E-01	3 Unchanged High
O15145	F10ab2	actin related protein 2/3 complex	3065.881	3190	1793.813	2683.638	-7.73E-01	5.78E-02	3 Unchanged High
P02570	A01cd7	actin; beta	66304.81	45400	38777.92	50171.41	-7.74E-01	-5.45E-01	3 Unchanged High
P02570	H12cd7	actin; beta	64949.74	42400	44598.66	50643.44	-5.42E-01	-6.16E-01	3 Unchanged High
P02570	P12cd7	actin; beta	21347.36	12200	15408.61	16331.85	-4.70E-01	-8.03E-01	3 Unchanged High
P02571	A06ab6	actin; gamma 1	69165.16	59100	65677.15	64643.45	-7.47E-02	-2.27E-01	3 Unchanged High
P12814	E23ab2	actinin; alpha 1	2400.607	2160	2638.011	2400.844	1.36E-01	-1.50E-01	3 Unchanged High
O43707	G05ab2	actinin; alpha 4	6999.138	3810	3499.234	4769.196	-1.00E+00	-8.78E-01	3 Unchanged High
P53999	C05cd7	activated RNA polymerase II Itau	4478.966	4320	6009.318	4936.98	4.24E-01	-1.13E-02	3 Unchanged High
P18848	I03ef5	activating transcription factor 4 (I	7160.888	5420	7668.286	6749.873	9.88E-02	-4.02E-01	3 Unchanged High
P53680	A07ef1	adaptor-related protein complex	2255.235	2530	4102.633	2963.423	8.63E-01	1.67E-01	3 Unchanged High
P29274	A16ef5	adenosine A2a receptor	1990.124	2960	2004.596	2318.367	1.05E-02	5.73E-01	3 Unchanged High
P54819	A04ab2	adenylate kinase 2	2997.607	2520	2851.739	2788.3	-7.20E-02	-2.53E-01	3 Unchanged High
Q01518	O18cd6	adenylyl cyclase-associated pro	6946.788	11000	7171.205	8362.375	4.59E-02	6.59E-01	3 Unchanged High
P32889	C03ef6	ADP-ribosylation factor 1	6040.796	7220	7907.02	7056.851	3.88E-01	2.58E-01	3 Unchanged High
P18085	P21ab2	ADP-ribosylation factor 4	4777.904	8880	8342.165	7331.81	8.04E-01	6.93E-01	3 Unchanged High
P26437	B02ab2	ADP-ribosylation factor 5	3739.477	4430	3984.845	4052.282	9.17E-02	2.45E-01	3 Unchanged High
Q9BZ4X	L08gh6	AKAP-binding sperm protein nsp	2345.455	2780	2500.118	2541.066	9.21E-02	2.44E-01	3 Unchanged High
P11766	K01ab2	alcohol dehydrogenase 5 (class I	2220.156	1990	2854.318	2354.247	3.62E-01	-1.59E-01	3 Unchanged High
P05067	N03ef6	amyloid beta (A4) precursor prot	2848.65	4180	3918.595	3649.558	4.61E-01	5.55E-01	3 Unchanged High
Q06481	K22ab2	amyloid beta (A4) precursor-like	2117.652	3230	2290.191	2546.598	1.13E-01	6.10E-01	3 Unchanged High
P07355	H12ab2	annexin A2	74767.39	112000	97217.17	94734.13	3.79E-01	5.86E-01	3 Unchanged High
P08758	I18ab2	annexin A5	4487.905	4270	7134.202	5295.976	6.69E-01	-7.32E-02	3 Unchanged High
P55064	O08ab2	aquaporin 5	10851.57	14200	11650.24	12248.87	1.02E-01	3.93E-01	3 Unchanged High
Q13520	O10ab2	aquaporin 6; kidney specific	2404.748	2350	2457.278	2404.397	3.12E-02	-3.25E-02	3 Unchanged High
P32391	D19ab2	ARP3 actin-related protein 3 hon	4291.823	4280	3941.05	4171.013	-1.23E-01	-3.92E-03	3 Unchanged High
O43776	E16ab7	asparaginyl-tRNA synthetase	2570.968	3010	2854.989	2811.634	1.51E-01	2.27E-01	3 Unchanged High
P24539	N22ab2	ATP synthase; H+ transporting; r	2908.697	3800	3228.203	3312.717	1.50E-01	3.86E-01	3 Unchanged High
P48201	P04ab2	ATP synthase; H+ transporting; r	5694.182	4370	4857.955	4974.135	-2.29E-01	-3.82E-01	3 Unchanged High
P05496	N24ab2	ATP synthase; H+ transporting;	2176.378	1760	2400.575	2112.628	1.41E-01	-3.06E-01	3 Unchanged High
Q06055	P02ab2	ATP synthase; H+ transporting;	5784.579	3530	7732.552	5682.609	4.19E-01	-7.12E-01	3 Unchanged High
O75947	P14ab2	ATP synthase; H+ transporting;	2668.028	2520	1881.974	2355.858	-5.04E-01	-6.37E-02	3 Unchanged High
P56385	P06ab2	ATP synthase; H+ transporting;	2682.798	2090	2616.726	2462.524	-3.60E-02	-3.62E-01	3 Unchanged High
P56134	P10ab2	ATP synthase; H+ transporting;	11587.91	17200	14181.18	14327.12	2.91E-01	5.71E-01	3 Unchanged High
P18859	P08ab2	ATP synthase; H+ transporting;	3879.839	4840	5176.982	4633.559	4.16E-01	3.20E-01	3 Unchanged High
O75964	P16ab2	ATP synthase; H+ transporting;	2021.591	2630	2009.026	2219.11	8.99E-03	3.78E-01	3 Unchanged High
P25705	N14ab2	ATP synthase; H+ transporting;	3657.512	2410	2967.207	3009.915	-3.02E-01	-6.05E-01	3 Unchanged High
P06576	N16ab2	ATP synthase; H+ transporting;	4072.978	3280	2557.982	3305.047	-6.71E-01	-3.11E-01	3 Unchanged High
P36542	N16ab2	ATP synthase; H+ transporting;	2479.5	2030	2436.284	2313.989	-2.54E-02	-2.91E-01	3 Unchanged High
P48047	P18ab2	ATP synthase; H+ transporting;	4222.314	4100	3541.047	3955.838	-2.54E-01	-4.09E-02	3 Unchanged High
Q01614	P01ef5	ATPase; Ca++ transporting; plas	3157.447	3180	3242.707	3193.535	3.84E-02	1.05E-02	3 Unchanged High
O99437	A11ab3	ATPase; H+ transporting; lysos	2495.618	3870	2087.291	2817.803	-2.58E-01	6.33E-01	3 Unchanged High
P36543	A09ab3	ATPase; H+ transporting; lysos	1854.198	2920	1659.749	2145.908	-1.60E-01	6.57E-01	3 Unchanged High
O75348	A15ab3	ATPase; H+ transporting; lysos	2734.484	5660	2721.878	3704.42	-6.67E-03	1.05E+00	3 Unchanged High
Q16864	A21ab3	ATPase; H+ transporting; lysos	6452.29	15900	7960.234	10101.59	3.03E-01	1.30E+00	3 Unchanged High
P27449	A05ab3	ATPase; H+ transporting; lysos	17134.14	24300	13120.57	18185.04	-3.85E-01	5.04E-01	3 Unchanged High
O00244	L14ab2	ATX1 antioxidant protein 1 homo	2833.957	3500	3977.547	3435.675	4.89E-01	3.03E-01	3 Unchanged High
O14503	M18ab3	basic helix-loop-helix domain cor	4978.916	4280	3254.631	4169.761	-6.13E-01	-2.20E-01	3 Unchanged High
O62038	L11ab5	BCL2/adenovirus E1B 19kD Inter	1473.428	2420	3224.141	2371.407	1.13E+00	7.14E-01	3 Unchanged High
P30536	L21ab3	benzodiazepine receptor (periph)	1997.929	2890	2326.211	2405.625	2.19E-01	5.34E-01	3 Unchanged High
P01884	C23ab3	bela-2-microglobulin	64872	105000	36055.95	68476.91	-8.47E-01	6.88E-01	3 Unchanged High
P22004	I13ab5	bone morphogenetic protein 6	5036.885	4710	3780.005	4509.317	-4.14E-01	-9.65E-02	3 Unchanged High
O95415	B02ef3	brain protein I3	7498.734	11200	5348.84	8032.295	-4.87E-01	5.95E-01	3 Unchanged High
O75531	K11ab3	Breakpoint cluster region protein	2541.769	2740	2924.826	2736.992	2.03E-01	1.11E-01	3 Unchanged High
P02593	A10ab6	calmodulin 2 (phosphorylase kinase)	1573.77	4130	4742.485	3482.215	1.59E+00	1.39E+00	3 Unchanged High
P07384	O24ef1	calpain 1; (mu/l) large subunit	3429.132	3420	2390.011	3078.324	-5.21E-01	-5.61E-03	3 Unchanged High
P27797	P05ab5	cathepsin L	10259.42	9700	1543.375	11797.33	5.89E-01	-8.16E-02	3 Unchanged High
P47756	N14ab4	CaM-KII inhibitory protein	20298.71	28200	21760.79	23425.99	1.00E-01	4.75E-01	3 Unchanged High
P15086	H13ab5	capping protein (actin filament) n	4348.079	4450	5015.377	4604.9	2.06E-01	3.38E-02	3 Unchanged High
P52952	D22ab5	CD24 antigen (small cell lung car	21319.27	27.1	26.97129	3273.378	-8.50E-01	-8.49E+00	3 Unchanged High
P13862	M21ef1	caselin kinase 2; beta polypeptid	3674.921	1740	2282.546	2292.94	-3.25E-01	-7.19E-01	3 Unchanged High
O14675	I02ef6	CASP8 and FADD-like apoptosi	2622.586	3840	3873.228	3795.282	7.58E-02	6.25E-02	3 Unchanged High
P35221	C17ef7	catenin (cadherin-associated pro	3813.516	2500	1151.661	2092.229	-1.19E+00	-6.77E-02	3 Unchanged High
P07858	E01ab5	cathepsin B	2480.797	4230	3300.738	3782.772	-2.08E-01	1.51E-01	3 Unchanged High
P48509	K16ab4	CD151 antigen	7267.56	3860	4485.422	3607.853	8.54E-01	6.37E-01	3 Unchanged High
P25063	G22cd8	CD24 antigen (small cell lung car	21319.27	13700	8768.731	9901.71	2.71E-01	9.11E-01	3 Unchanged High
P16070	O21ef1	CD44 antigen (homing function	16178.96	18200	8278.973	15932.79	-1.36E+00	-2.28E-01	3 Unchanged High
P08962	O18ab4	CD53 antigen (melanoma 1 anti-	9354.914	9640	5778.642	10533.43	-1.49E+00	-7.47E-01	3 Unchanged High
O14519	K04ef5	CDK2-associated protein 1	4231.191	11600	1001629	10307.1	9.86E-02	3.04E-01	3 Unchanged High
P25763	A12ab6	cell division cycle 42 (GTP bindi	4588.819	4180	4763.013	4389.995	1.71E-01	-1.90E-02	3 Unchanged High
P49368	N17cd2	chaperonin containing TCP1; sub	2356.627	2840	2852.186	3426.736	-6.66E-01	-6.93E-01	3 Unchanged High
P48643	H10ef4	chaperonin containing TCP1; sub	2238.933	2880	2222.361	2484.939	-8.46E-02	2.87E-01	3 Unchanged High
O00289	M19ab8	chloride intracellular channel 1	6811.55	2330	1561.625	2042.12	-5.20E-01	5.49E-02	3 Unchanged High
Q9Y2Q7	N02cd8	chromosome 11 open reading fr	4087.361	7240	5727.121	6591.299	-2.50E-01	8.71E-02	3 Unchanged High
P09496	F15ab5	clathrin; light polypeptide (Lca)	5758.632	3800	5946.259	4610.942	5.41E-01	-1.05E-01	3 Unchanged High
O95832	L04gh1	claudin 1	3046.376	9260	5849.641	6957.341	2.26E-02	6.86E-01	3 Unchanged High
O95471	A13ef1	claudin 7	2688.819	2450	818.083	2138.383	-1.73E+00	-3.14E-01	3 Unchanged High
				3350	1520.977	2587.177	-9.25E-01	2.14E-01	3 Unchanged High

Q9UII4	B14ef1	cyclin-E binding protein 1	26180.8	29800	39655.02	31877.4	5.99E-01	1.87E-01	3 Unchanged High
P04080	G16ab3	cystatin B (stein B)	4312.168	5420	2307.13	4034.272	-8.63E-01	3.30E-01	3 Unchanged High
P21291	J01ab5	cysteine and glycine-rich protein	2478.36G	1710	2135.86	2109.096	-2.15E-01	-5.33E-01	3 Unchanged High
O00622	J15er7	cysteine-rich; angiogenic inducer	2070.203	1620	2978.542	2224.339	5.25E-01	-3.50E-01	3 Unchanged High
P13073	L19ab5	cytochrome c oxidase subunit IV	6219.628	8550	6571.848	7115.048	7.95E-02	4.60E-01	3 Unchanged High
P12074	K13gh1	cytochrome c oxidase subunit VII	3253.24	5800	4244.557	4434.13	3.84E-01	8.35E-01	3 Unchanged High
Q02221	E17ab6	cytochrome c oxidase subunit VII	2968.24	2820	4604.241	3464.904	6.33E-01	-7.28E-02	3 Unchanged High
P14854	A20ab6	cytochrome c oxidase subunit VII	1991.91	2650	2380.795	2344.331	2.57E-01	4.17E-01	3 Unchanged High
P09669	E12ab6	cytochrome c oxidase subunit VII	2580.598	2090	1927.002	2197.58	-4.21E-01	-3.08E-01	3 Unchanged High
P14406	G02ab5	cytochrome c oxidase subunit VII	4846.713	4500	4245.478	4530.346	-1.91E-01	-1.07E-01	3 Unchanged High
O14548	G23cd5	cytochrome c oxidase subunit VII	2182.954	2450	3040.586	2556.481	4.78E-01	1.64E-01	3 Unchanged High
P24311	K17ab5	cytochrome c oxidase subunit VII	3224.558	5150	3801.752	4057.995	2.38E-01	6.75E-01	3 Unchanged High
P15954	P04ab5	cytochrome c oxidase subunit VII	12335.74	12200	9883.688	11482.48	-3.20E-01	-1.27E-02	3 Unchanged High
P01017	B10ab5	cytochrome c oxidase subunit VII	3019.162	1900	3329.281	2750.974	1.41E-01	-6.65E-01	3 Unchanged High
O43293	K19ab4	death-associated protein kinase	2535.403	1650	2088.808	2157.783	-2.80E-01	-4.55E-01	3 Unchanged High
P46956	G14ef6	defender against cell death 1	7921.682	11200	9546.898	9563.241	2.69E-01	5.02E-01	3 Unchanged High
Q09753	G01ab6	defensin; beta 1	4071.982	7630	2153.638	4619.611	-9.19E-01	9.07E-01	3 Unchanged High
P18282	F23ab2	desmin (actin depolymerizing factor)	7729.126	7570	6083.408	7126.01	-3.45E-01	-3.09E-02	3 Unchanged High
P07108	H04gh1	diacetate binding inhibitor (GAB)	2541.011	1730	2995.768	2422.578	2.38E-01	-5.54E-01	3 Unchanged High
P31689	D18ab7	DnaJ (Hsp40) homolog; subfamily	2491.051	2930	1789.662	2402.398	-4.77E-01	2.32E-01	3 Unchanged High
Q9Y5T4	I10cd8	DNAJ domain-containing	2324.933	2520	2397.896	2414.457	4.46E-02	1.17E-01	3 Unchanged High
Q9Y4E3	G15cd5	dual-specific tyrosine-(Y)-phos	8211.965	6870	5987.39	7023.599	-4.56E-01	-2.57E-01	3 Unchanged High
Q9NP97	C02ef8	dynelin light chain 2A	4080.949	4160	5365.928	4534.283	3.95E-01	2.63E-02	3 Unchanged High
Q15701	L08cd3	dynelin; cytoplasmic; light polypept	4492.679	5800	4332.161	4975.685	-5.25E-02	3.69E-01	3 Unchanged High
P78545	O16ab4	E74-like factor 3 (ets domain) trar	3781.196	2780	1455.944	2673.744	-1.38E+00	-4.42E-01	3 Unchanged High
O60869	A03cd4	endothelial differentiation-related	5515.692	5680	4090.527	5094.856	-4.31E-01	4.19E-02	3 Unchanged High
Q14259	L06ab4	enhances of rudimentary homeobox	3593.608	3950	5175.131	4241.036	5.26E-01	1.38E-01	3 Unchanged High
P06733	C16ab4	endolase 1; ( $\alpha$ )	12539.397	7460	9955.024	9983.774	-3.33E-01	-7.50E-01	3 Unchanged High
P22712	D11gh6	endolase 1; ( $\alpha$ )	6900.857	4290	5016.695	5403.444	4.60E-01	-6.65E-01	3 Unchanged High
P04720	O07ab6	eukaryotic translation elongation	36222.34	23200	23485.94	27648.74	-6.25E-01	-6.40E-01	3 Unchanged High
P26641	A10ab4	eukaryotic translation elongation	6863.565	6540	11607.61	8337.901	7.58E-01	-6.91E-02	3 Unchanged High
P13639	I15ab5	eukaryotic translation elongation	4023.855	2310	3360.073	3231.325	-2.60E-01	-8.01E-01	3 Unchanged High
O15372	L24cd3	eukaryotic translation initiation f	2870.027	1930	2391.869	2398.394	-2.63E-01	5.70E-01	3 Unchanged High
O75821	L22cd3	eukaryotic translation initiation f	3009.075	2670	3333.728	3005.577	1.48E-01	-1.70E-01	3 Unchanged High
Q64252	L11ab6	eukaryotic translation initiation f	2755.438	1540	2127.874	2141.68	-3.73E-01	-8.38E-01	3 Unchanged High
O15371	L18cd3	eukaryotic translation initiation f	4273.919	4030	3558.838	3954.374	-2.64E-01	-8.46E-02	3 Unchanged High
P04765	A22ab4	eukaryotic translation initiation f	7716.222	7170	6363.169	7083.99	-2.78E-01	-1.05E-01	3 Unchanged High
Q14240	H13ab4	eukaryotic translation initiation f	2091.816	2190	2519.322	2267.015	2.68E-01	6.61E-02	3 Unchanged High
P10159	A18ab5	eukaryotic translation initiation f	9023.244	5240	5651.752	6638.65	-6.75E-01	-7.84E-01	3 Unchanged High
Q9NQT4	H05gh4	exosome component Rrp46	2098.514	2590	2304.48	2331.056	1.35E-01	3.04E-01	3 Unchanged High
P02794	C12ab6	ferritin; heavy polypeptide 1	35912.81	48700	42075.22	42243.59	2.28E-01	4.41E-01	3 Unchanged High
P02792	M10ab3	ferritin; light polypeptide	44225.86	29600	17849.2	30568.13	-1.31E+00	-5.78E-01	3 Unchanged High
Q05472	B02ab4	Finkel-Biskis-Reilly murine sarco	10322.94	10400	9704.642	10145.46	-8.91E-01	1.19E-02	3 Unchanged High
P20071	F08ab3	FKS06 binding protein 1A (12kD)	2741.389	1870	1414.949	2009.291	-9.54E-01	-5.51E-01	3 Unchanged High
P50395	J02ab4	GDP dissociation inhibitor 2	2287.713	1580	2291.27	2051.41	2.24E-03	-5.38E-01	3 Unchanged High
P48507	E12ab5	glutamate-cysteine ligase; modifi	154.173	762	5937.375	2055.914	5.27E+00	-1.02E+00	3 Unchanged High
P36969	D14ab5	glutathione peroxidase 4 (phos)	3397.2	4860	3108.036	3787.13	-1.28E-01	5.15E-01	3 Unchanged High
P09211	L10ab3	glutathione S-transferase pi	6392.334	8570	4067.789	6378.198	-6.52E-01	4.40E-01	3 Unchanged High
P04406	A01cd8	glyceraldehyde-3-phosphate deh	28809.37	38300	44655.67	37260.67	6.32E-01	4.11E-01	3 Unchanged High
P04406	H12cd8	glyceraldehyde-3-phosphate deh	37562.25	60200	57135.41	51621.55	6.05E-01	6.80E-01	3 Unchanged High
P120d8		glyceraldehyde-3-phosphate deh	12053.5	14900	19061.52	15342.7	6.61E-01	3.07E-01	3 Unchanged High
P43304	H01ab3	glycerol-3-phosphate dehydroge	3450.634	2340	3276.264	3023.392	-7.48E-02	-5.58E-01	3 Unchanged High
P41250	F02ef7	glycyl-tRNA synthetase	4333.439	3630	6248.604	4736.632	5.28E-01	-2.56E-01	3 Unchanged High
P04895	K17ef5	GNAS complex locus	7755.658	9290	9107.558	8718.93	2.32E-01	2.61E-01	3 Unchanged High
P24522	S03ef6	growth arrest and DNA-damage-1	2792.429	6130	3396.736	4105.138	2.83E-01	1.13E+00	3 Unchanged High
Q92847	M24ab5	growth hormone secretagogue re	2827.902	2100	2597.123	2508.414	-1.23E-01	-4.29E-01	3 Unchanged High
P04901	B01ef1	guanine nucleotide binding prote	5734.337	7610	5853.112	6398.85	2.95E-02	4.08E-01	3 Unchanged High
P25388	E20cd6	guanine nucleotide binding prote	22430.28	15300	19055.7	18939.85	-2.35E-01	-5.49E-01	3 Unchanged High
P06351	G08ab6	H3 histone; family 3B (H3.3B)	2448.264	2770	2042.864	2421.658	-2.61E-01	1.80E-01	3 Unchanged High
P04792	A16ef5	heat shock 27kD protein 1	41952.14	34500	31970.86	36135.19	-3.92E-01	-2.83E-01	3 Unchanged High
R11021	H01ef1	heat shock 70kD protein 5 (gluc)	3226.183	1600	4101.742	2976.537	3.46E-01	-1.01E+00	3 Unchanged High
P38646	O19ab7	heat shock 70kD protein 98 (nor	2861.743	2180	2220.509	2417.791	-3.61E-01	-3.87E-01	3 Unchanged High
Q9U7K6	J14ef1	hematological and neurological e	26342.33	35400	41099.58	34285.74	6.42E-01	4.27E-01	3 Unchanged High
P09651	F12ab7	heterogeneous nuclear ribonucle	2522.253	1650	2524.082	2231.413	1.05E-03	-6.14E-01	3 Unchanged High
Q9Y4J5	I23ef1	heterogeneous nuclear ribonucle	3825.912	2370	3770.457	3320.487	-2.11E-02	-6.94E-01	3 Unchanged High
P09429	F10ab7	high-mobility group (nonhistone	2534.273	1660	3502.047	2567.093	4.67E-01	-6.66E-01	3 Unchanged High
P49773	M03ef6	histidine triad nucleotide binding	6025.978	7790	7379.267	7064.436	2.92E-01	3.70E-01	3 Unchanged High
Q92769	N05ab4	histone deacetylase 2	2454.324	2220	1789.508	2155.575	-5.46E-01	-1.43E-01	3 Unchanged High
P17693	F08ab7	HLA-G Histocompatibility antigen	2048.009	2780	1844.177	2225.106	-1.51E-01	4.42E-01	3 Unchanged High
P17483	C15gh2	homeo box 84	2892.488	3490	2902.69	3095.004	5.08E-03	2.71E-01	3 Unchanged High
Q9UL99	C01cd8	hyaluronoglucosaminidase 4	3623.461	2050	2169.656	2621.266	-7.27E-01	-8.21E-01	3 Unchanged High
Q9GZT3	L18gh7	hypothetical protein DC50	3343.922	3750	4298.676	3797.943	3.62E-01	1.66E-01	3 Unchanged High
Q9NVW5	O12gh2	hypothetical protein FLJ20533	3104.471	5460	6184.227	4915.419	9.94E-01	8.14E-01	3 Unchanged High
Q9U130	P08ef2	hypothetical protein HSPC152	3000.217	4060	4396.662	3819.313	5.51E-01	4.37E-01	3 Unchanged High
Q9BQB6	P08gh5	hypothetical protein IMAGE3455:	3599.509	5410	8667.307	5897.337	1.27E+00	5.87E-01	3 Unchanged High
Q9BWJ5	P18gh7	hypothetical protein MGC3133	2074.073	2520	2719.671	2436.767	3.91E-01	2.79E-01	3 Unchanged High
Q9Y683	N11ef2	hypothetical protein MGC8721	2425.475	2730	2939.253	2699.545	2.77E-01	1.73E-01	3 Unchanged High
Q16665	P01ef6	hypoxia-inducible factor 1; alpha	3544.753	2960	1526.935	2675.668	-1.22E+00	-2.62E-01	3 Unchanged High
O75353	G04ef6	immediate early response 3	4564.408	4690	3129.721	4129.098	-5.44E-01	4.01E-02	3 Unchanged High
Q16270	J15ab6	insulin-like growth factor binding	6185.622	21800	18047.34	15334.47	1.54E+00	1.82E+00	3 Unchanged High
Q9Y287	A03gh2	integral membrane protein 2B	6908.997	10500	10014.47	9139.933	5.36E-01	6.03E-01	3 Unchanged High
P56537	D16ab6	integrin beta 4 binding protein	2594.316	3270	1568.747	2476.062	-7.26E-01	3.32E-01	3 Unchanged High
P26006	D08ab6	integrin; alpha 3 (antigen CD49C)	2669.777	2740	1339.712	2249.026	-9.95E-01	3.62E-02	3 Unchanged High

Q13907	A24ab7	isopentenyl-diphosphate delta Is:	2958.139	1660	2475.365	2362.933	-2.57E-01	-8.38E-01	3	Unchanged	High
P33947	K03cd7	KDEL (Lys-Asp-Glu-Leu) endopl	1667.246	1250	3924.993	2261.692	1.24E+00	-4.12E-01	3	Unchanged	High
P00338	D15ab7	lactate dehydrogenase A	44091.29	34500	42150.03	40260.24	-6.46E-02	-3.52E-01	3	Unchanged	High
P08865	G21ef7	laminin receptor 1 (67kD; ribosor	8548.245	6070	9921.409	8180.607	2.15E-01	-4.93E-01	3	Unchanged	High
Q08380	D17eb7	lectin; galactoside-binding; solub	2294.491	2850	3014.02	2719.794	3.94E-01	3.13E-01	3	Unchanged	High
O14949	F17ef3	low molecular mass ubiqunone-t	2942.579	3550	3637.463	3377.305	3.06E-01	2.71E-01	3	Unchanged	High
Q15012	F20ef4	lysosomal-associated protein tra	2815.002	4690	5453.634	4319.567	9.54E-01	7.36E-01	3	Unchanged	High
P14174	J05ef7	macrophage migration inhibitory	5544.722	6700	6763.718	6337.062	2.87E-01	2.74E-01	3	Unchanged	High
P49006	M05ef6	macrophage myristoylated alanyl	5857.382	10400	6986.315	6400.725	6.17E-01	8.22E-01	3	Unchanged	High
P30463	G10ab6	major histocompatibility complex;	2701.757	4890	2255.929	3281.592	-2.60E-01	8.55E-01	3	Unchanged	High
P10321	A01cd2	major histocompatibility complex;	8949.086	17000	10196.88	12044.89	1.88E-01	9.25E-01	3	Unchanged	High
P10321	H12cd2	major histocompatibility complex;	7167.905	21600	11111.54	13298.19	6.28E-01	1.59E+00	3	Unchanged	High
P10321	P12cd2	major histocompatibility complex;	13121.35	16800	11725.68	13868.02	-1.62E-01	3.53E-01	3	Unchanged	High
P13747	M24ab7	major histocompatibility complex;	2540.911	2790	2053.351	2460.503	-3.07E-01	1.33E-01	3	Unchanged	High
Q95HC0	P02gh6	major histocompatibility complex;	5067.294	4140	3295.115	4168.835	-6.21E-01	-2.90E-01	3	Unchanged	High
P13640	D13gh6	metallothionein 1G	6180.376	4750	2940.683	4624.849	-1.07E+00	-3.79E-01	3	Unchanged	High
P80297	D17gh6	metallothionein 1X	4881.982	5310	5233.749	5142.996	1.005E-01	1.22E-01	3	Unchanged	High
P02795	L04ab7	metallothionein 2A	6620.235	7330	8067.274	7340.215	2.85E-01	1.48E-01	3	Unchanged	High
P14880	ED4ab7	microsomal glutathione S-transferase	5023.542	7940	4177.165	5712.043	-2.65E-01	6.60E-01	3	Unchanged	High
Q9NYZ2	M22ef2	mitochondrial solute carrier	2488.07	2850	2240.824	2527.436	-1.51E-01	1.98E-01	3	Unchanged	High
P26038	K05eb7	moesin	4260.51	4580	3801.298	4212.427	-1.65E-01	1.03E-01	3	Unchanged	High
O15329	O12ef1	mucin 6; gastric	5574.093	5950	6685.047	6068.269	2.62E-01	9.31E-02	3	Unchanged	High
P16475	J02gh1	myosin; light polypeptide 6; alkal	48122.62	45200	48882.54	47407.02	2.26E-02	8.99E-02	3	Unchanged	High
P19105	N03cd6	myosin; light polypeptide; regulat	7920.873	8150	7228.401	7764.994	-1.32E-01	4.04E-02	3	Unchanged	High
Q9UIC23	D06ef1	N-acetylglucosamine-1-phospho	1884.596	2680	2511.293	2357.087	4.14E-01	5.05E-01	3	Unchanged	High
O15239	E22ab7	NADH dehydrogenase (ubiquinol	2859.738	5440	3719.503	4005.894	3.79E-01	9.27E-01	3	Unchanged	High
000483	J02ab7	NADH dehydrogenase (ubiquinol	5214.222	5540	9086.615	6613.046	8.01E-01	8.70E-02	3	Unchanged	High
O75438	J04ab8	NADH dehydrogenase (ubiquinol	1628.024	2170	2842.647	2212.932	8.04E-01	4.13E-01	3	Unchanged	High
O95168	J08ab8	NADH dehydrogenase (ubiquinol	2297.787	3270	2253.854	2607.423	-2.79E-02	5.09E-01	3	Unchanged	High
O95298	J12ab8	NADH dehydrogenase (ubiquinol	1909.371	2840	2888.281	2544.679	5.97E-01	5.71E-01	3	Unchanged	High
O43920	J18ab8	NADH dehydrogenase (ubiquinol	6241.135	11500	8014.187	8594.08	3.61E-01	8.85E-01	3	Unchanged	High
O13765	H09ab7	nascent-polypeptide-associat	2800.535	3390	3897.956	3363.371	4.77E-01	2.76E-01	3	Unchanged	High
Q15843	K13cd1	neural precursor cell expressed;	3449.484	4710	4139.56	4098.747	2.63E-01	4.48E-01	3	Unchanged	High
Q9NX14	C01gh3	neuronal protein 17.3	3476.812	3150	5077.834	3902.8	5.46E-01	-1.41E-01	3	Unchanged	High
Q9YR26	F18gh6	NICE-3 protein	1763.974	2250	2329.521	2113.511	4.01E-01	3.49E-01	3	Unchanged	High
Q15668	H13cd6	Niemann-Pick disease; type C2	1516.592	3640	2828.255	2662.845	8.99E-01	1.26E+00	3	Unchanged	High
O14597	J21ef4	non-functional folate binding pro	2917.293	2170	3004.012	2697.108	4.23E-02	-4.27E-01	3	Unchanged	High
P15531	E02ef5	non-metastatic cells 1; protein (N	6653.515	6940	7836.897	7143.349	2.36E-01	6.07E-02	3	Unchanged	High
P22392	L12cd2	non-metastatic cells 2; protein (N	4827.494	5680	4836.596	5114.664	2.72E-03	2.35E-01	3	Unchanged	High
O00746	D04ef7	non-metastatic cells 4; protein ex	2211.058	2270	4300.604	2927.223	9.60E-01	3.80E-02	3	Unchanged	High
O75534	B01cd4	NRAS-related gene	3478.657	3510	2737.425	3241.263	-3.46E-01	1.20E-02	3	Unchanged	High
Q9H9A1	C24gh6	nuclear receptor co-repressor/HC	5951.715	3290	2990.083	4076.544	-9.93E-01	-8.56E-01	3	Unchanged	High
Q9NPE3	K15ef1	nucleolar protein Family A; memb	3543.239	7130	3639.205	4771.656	3.86E-02	1.01E+00	3	Unchanged	High
P54368	G10ef1	ornithine decarboxylase antizym	7212.068	6880	7782.339	7292.818	1.10E-01	-6.72E-02	3	Unchanged	High
Q9UH52	L23cd8	over-expressed breast tumor pro	2335.527	2320	1884.264	2181.482	-3.10E-01	-6.73E-03	3	Unchanged	High
Q15070	A09cd1	oxidase (cytochrome c) assembly	2161.529	2500	1436.463	2031.796	-5.90E-01	2.08E-01	3	Unchanged	High
Q9H230	G14gh5	p53-induced protein PTGPC1	1823.554	3330	1443.914	2199.367	-3.37E-01	8.69E-01	3	Unchanged	High
O60356	M03cd8	p68 protein (candidate of metasta	1774.942	1940	2740.792	2150.631	6.27E-01	1.25E-01	3	Unchanged	High
P78337	M22ab8	paired-like homeodomain transcr	15428.96	13300	14490.63	14411.94	-9.05E-02	-2.12E-01	3	Unchanged	High
Q9C086	P20gh7	PAP-1 binding protein	2992.2	3610	5014.215	3872.969	7.45E-01	2.72E-01	3	Unchanged	High
Q15165	D06ef6	paraoxonase 2	1325.972	3740	2122.119	2394.717	6.78E-01	1.49E+00	3	Unchanged	High
P20962	N13ab8	peptidylprolyl isomerase B (cydo	2345.869	2330	3489.616	2722.317	5.73E-01	-8.88E-03	3	Unchanged	High
P23284	I17ab8	peptidylprolyl isomerase B (cydo	5298.839	5860	8890.43	6683.166	7.47E-01	1.45E-01	3	Unchanged	High
Q06830	E18ab8	peroxiredoxin 1	2973.862	2450	2056.112	2493.75	-5.32E-01	-2.79E-01	3	Unchanged	High
P32119	G04ef7	peroxiredoxin 2	3141.718	3330	2921.471	3130.835	-1.05E-01	8.37E-02	3	Unchanged	High
P30048	N09ab2	peroxiredoxin 3	2420.936	2010	1671.796	2035.218	-5.34E-01	-2.66E-01	3	Unchanged	High
Q13162	N07ab2	peroxiredoxin 4	2744.707	2080	3645.718	2822.139	4.10E-01	-4.03E-01	3	Unchanged	High
P30044	P15cd7	peroxiredoxin 5	2205.14	3820	1714.041	2581.24	-3.63E-01	7.94E-01	3	Unchanged	High
Q13492	B13cd4	phosphatidylinositol binding clat	2688.917	2690	1861.508	2414.998	-5.31E-01	3.03E-03	3	Unchanged	High
P08237	P02ab7	phosphofructokinase; muscle	2790.708	1980	2829.743	2533.875	2.00E-02	4.94E-01	3	Unchanged	High
P00558	P06ab7	phosphoglycerate kinase 1	5186.346	5130	6341.68	5552.736	2.90E-01	-1.57E-02	3	Unchanged	High
P16669	K14ab8	phosphoglycerate mutase 1 (bra)	1847.463	2730	2859.446	2477.75	6.30E-01	5.61E-01	3	Unchanged	High
Q14801	B01cd8	phosphoprotein enriched in astr	2326.556	17400	19729.36	20128.93	-2.39E-01	-4.23E-01	3	Unchanged	High
O14832	A04cd1	phytanoyl-CoA hydroxylase (Ref)	7333.104	7780	8341.917	7819.036	1.86E-01	8.57E-02	3	Unchanged	High
P53801	L01ef1	pituitary tumor-transforming 1 int	4385.308	5330	4172.137	4627.881	-7.19E-02	2.80E-01	3	Unchanged	High
Q9HB21	E19gh5	pleckstrin homology domain-cont	2318.08	3070	2907.381	2766.359	3.27E-01	4.07E-01	3	Unchanged	High
Q15365	O09cd1	poly(R3C) binding protein 1	4617.635	3130	3156.644	3635.431	-5.49E-01	-5.60E-01	3	Unchanged	High
P52433	B17ab8	polymerase (RNA) II (DNA direct	2157.353	3780	3657.763	3198.285	7.62E-01	8.09E-01	3	Unchanged	High
P52436	L16gh1	polymerase (RNA) II (DNA direct	2161.398	2600	2709.495	2489.343	3.26E-01	2.65E-01	3	Unchanged	High
Q3052	B19ab8	POU domain; class 3; transcript	3321.206	2650	2251.677	2740.913	-5.61E-01	-3.26E-01	3	Unchanged	High
	K20gh5	PP1201 protein	7127.293	6650	2688.636	5487.085	-1.41E+00	-1.01E-01	3	Unchanged	High
P40425	G08ab8	pre-B-cell leukemia transcription	2817.191	2650	3413.81	2958.976	2.77E-01	-9.05E-02	3	Unchanged	High
Q99471	K06ab8	prefoldin 5	1827.777	2160	2837.334	2275.038	6.34E-01	2.41E-01	3	Unchanged	High
Q9UHZ2	E21ef8	PRO1073 protein	1872.208	3140	1690.101	2234.209	-1.48E-01	7.46E-01	3	Unchanged	High
P07737	A21cd1	profilin 1	29650.38	48900	35394.8	37970.06	2.55E-01	7.21E-01	3	Unchanged	High
Q92740	E03gh1	prosaposin (variant Gaucher dise	4235.232	5370	4268.459	4622.898	1.13E-02	3.41E-01	3	Unchanged	High
P07478	N02cd2	protease; serine; 2 (trypsin 2)	77359.27	42600	51746.68	57240.67	-5.80E-01	-8.60E-01	3	Unchanged	High
Q9UL46	N09ab8	proteasome (prosome; macropal	3682.153	4550	2712.172	3648.995	-4.41E-01	3.06E-01	3	Unchanged	High
P25786	L09ef7	proteasome (prosome; macropal	2270.079	2570	2265.763	2369.437	-2.75E-03	1.80E-01	3	Unchanged	High
P20618	J17ab8	proteasome (prosome; macropal	2835.653	3590	2620.916	3082.003	-7.52E-03	3.40E-01	3	Unchanged	High
P49720	J21ab8	proteasome (prosome; macropal	1714.767	2100	2435.426	2081.991	5.06E-01	2.89E-01	3	Unchanged	High
P28070	J23ab8	proteasome (prosome; macropal	2193.138	1760	2224.325	2058.212	2.04E-02	-3.20E-01	3	Unchanged	High
Q99436	L03ab8	proteasome (prosome; macropal	4179.694	3450	3072.098	3566.368	-4.44E-01	-2.78E-01	3	Unchanged	High

Q15249	H13ef5	prothymosin; alpha (gene sequer	11382.44	14500	9974.587	11954.68	-1.90E-01	3.50E-01	3	Unchanged	High
Q9NQ11	G03gh7	putative ATPase	2774.724	2460	2271.593	2501.162	-2.89E-01	-1.75E-01	3	Unchanged	High
P41567	N06cd5	putative translation Initiation factor	7487.872	6600	8909.545	7666.779	2.51E-01	-1.81E-01	3	Unchanged	High
Q15181	L18gh1	pyrophosphatase (inorganic)	4914.897	4350	2667.605	3978.537	-8.82E-01	-1.75E-01	3	Unchanged	High
P14786	M24ab8	pyruvate kinase; muscle	6305.222	8060	9000.504	7787.922	5.13E-01	3.54E-01	3	Unchanged	High
P57735	G12gh4	RAB25; member RAS oncogene	3343.628	4890	1366.379	3198.699	-1.29E+00	5.47E-01	3	Unchanged	High
P54725	E21cd1	RAD23 homolog A ( <i>S. cerevisiae</i> )	2533.36	1790	1753.113	2026.126	-6.31E-01	-5.00E-01	3	Unchanged	High
P54727	M10ef6	RAD23 homolog B ( <i>S. cerevisiae</i> )	4038.884	5410	4983.21	4809.132	3.03E-01	4.20E-01	3	Unchanged	High
O00538	P16od5	RAS guanyl releasing protein 2 (r	2418.688	2310	1906.199	2210.191	-3.44E-01	-6.90E-02	3	Unchanged	High
P06749	C21gh1	ras homolog gene family; membe	2136.708	1940	3003.841	2358.668	4.91E-01	-1.43E-01	3	Unchanged	High
P08134	B16ab2	ras homolog gene family; membe	4404.567	4490	2930.236	3943.029	-5.88E-01	2.91E-02	3	Unchanged	High
P06gh8	ras-like protein VTS58635		5451.542	6580	9066.798	7033.479	7.34E-01	2.72E-01	3	Unchanged	High
P15154	C01ef6	ras-related C3 botulinum toxin st	10849.13	9720	10044.19	10202.94	-1.11E-01	-1.59E-01	3	Unchanged	High
Q15247	B20cd5	ras-related GTP-binding protein	1728.963	2380	2623.418	2244.978	6.02E-01	4.63E-01	3	Unchanged	High
O95197	A06cd6	reticulon 3	3712.756	3420	3833.411	3654.06	4.61E-02	-1.20E-01	3	Unchanged	High
P09455	F12ab8	retinol binding protein 1; cellular	2211.12	4480	2383.274	3023.27	1.08E-01	1.02E+00	3	Unchanged	High
P52565	K13ef6	Rho GDP dissociation inhibitor (C	3166.04	3200	3141.434	3169.009	-1.13E-02	1.52E-02	3	Unchanged	High
P27635	N19cd2	ribosomal protein L10	13406.29	7100	11103.69	10536.25	-2.72E-01	-9.17E-01	3	Unchanged	High
P53025	G22cd1	ribosomal protein L10a	19374.73	15100	19939.26	18124.91	4.14E-02	-3.63E-01	3	Unchanged	High
P39026	D07cd1	ribosomal protein L11	14172.29	6760	10346.92	10427.07	-4.54E-01	-1.07E+00	3	Unchanged	High
P30050	D09cd1	ribosomal protein L12	38376.69	24500	38669.34	33860.13	1.10E-02	-6.45E-01	3	Unchanged	High
P40429	A01ef1	ribosomal protein L13a	23800.5	22200	28159.37	24735.85	2.43E-01	-9.73E-02	3	Unchanged	High
P50914	B18cd4	ribosomal protein L14	18507.36	14600	16108.18	16402.14	-2.00E-01	-3.43E-01	3	Unchanged	High
P39030	C13cd3	ribosomal protein L15	8407.532	8100	10809.12	9104.589	3.62E-01	-5.43E-02	3	Unchanged	High
P18621	D19cd1	ribosomal protein L17	8779.141	8440	10004.78	9074.166	1.89E-01	-5.71E-02	3	Unchanged	High
Q70702	D13cd1	ribosomal protein L18	12168.43	10200	15619.17	12658.45	3.60E-01	-2.56E-01	3	Unchanged	High
Q02543	C15gh1	ribosomal protein L18a	24976.59	27200	28170.19	26796.74	1.74E-01	1.25E-01	3	Unchanged	High
P14118	A15cd1	ribosomal protein L19	6226.589	5530	5535.643	5762.718	-1.70E-01	-1.72E-01	3	Unchanged	High
P46778	A13cd3	ribosomal protein L21	11156.59	11800	16742.21	13222.79	5.86E-01	7.72E-02	3	Unchanged	High
P35268	D17cd1	ribosomal protein L22	16289.45	16200	18991.35	17168.94	2.21E-01	-5.63E-03	3	Unchanged	High
P23131	F11cd4	ribosomal protein L23	20972.93	20400	25729.93	22356.23	2.95E-01	-4.24E-02	3	Unchanged	High
P29316	G09cd3	ribosomal protein L23a	6385.675	4840	5446.963	5556.302	-2.29E-01	-4.01E-01	3	Unchanged	High
P38663	D21cd1	ribosomal protein L24	7805.803	6180	5479.195	6488.503	-5.11E-01	-3.37E-01	3	Unchanged	High
P08526	F01cd1	ribosomal protein L27	12974.22	5280	10256.69	9469.252	-3.28E-01	-1.29E+00	3	Unchanged	High
P46776	F05cd1	ribosomal protein L27a	16046.37	17000	20949.85	18000.07	3.85E-01	8.57E-02	3	Unchanged	High
P46779	F07cd1	ribosomal protein L28	40540.59	32400	45810.52	39577.25	1.76E-01	-3.24E-01	3	Unchanged	High
P47914	E23cd3	ribosomal protein L29	3346.473	1960	1947.028	2417.223	-7.81E-01	-7.73E-01	3	Unchanged	High
P39023	B21cd1	ribosomal protein L3	13192.5	10500	13962.55	12535.38	8.18E-02	-3.36E-01	3	Unchanged	High
P04645	F03cd1	ribosomal protein L30	17693.61	12300	21530.83	17188.03	2.83E-01	-5.20E-01	3	Unchanged	High
P12947	F09cd1	ribosomal protein L31	9749.468	6980	12591.65	10441.63	3.69E-01	-1.18E-01	3	Unchanged	High
P02433	A15cd3	ribosomal protein L32	22774.44	24400	30742.77	25982.45	4.33E-01	1.01E-01	3	Unchanged	High
P49207	F11cd1	ribosomal protein L34	13251.1	11500	13193.66	12661.96	-6.27E-03	-1.99E-01	3	Unchanged	High
P42766	K16cd7	ribosomal protein L35	10454.27	10500	10655.65	10527.37	2.75E-02	2.47E-03	3	Unchanged	High
P18077	F13cd1	ribosomal protein L35a	14583.91	10700	8811.726	11356.13	-7.27E-01	-4.50E-01	3	Unchanged	High
P09895	J06gh1	ribosomal protein L36a	8395.644	8780	12052.18	9742.196	5.22E-01	6.44E-02	3	Unchanged	High
P09896	A19cd3	ribosomal protein L36a-like	5167.775	5750	4693.401	5203.379	-1.39E-01	1.54E-01	3	Unchanged	High
P02403	F15cd1	ribosomal protein L37	31895.4	45000	41301.54	39386.47	3.73E-01	4.95E-01	3	Unchanged	High
P12751	F17cd1	ribosomal protein L37a	18652.48	17300	19955.82	18651.98	9.74E-02	-1.05E-01	3	Unchanged	High
P23411	F19cd1	ribosomal protein L38	5149.82	5570	7560.21	6091.715	5.54E-01	1.12E-01	3	Unchanged	High
P02404	A17cd3	ribosomal protein L39	14114.05	21300	22827.16	19427.01	6.94E-01	5.96E-01	3	Unchanged	High
P36578	B23cd1	ribosomal protein L4	14367.47	10400	10448.85	11723.95	-4.59E-01	-4.72E-01	3	Unchanged	High
P28751	L06gh1	ribosomal protein L41	35135.75	34300	40372.62	36614.61	2.00E-01	-3.32E-02	3	Unchanged	High
P46777	E21cd3	ribosomal protein L5	12002.66	8880	10351.69	10411.06	-2.13E-01	-4.35E-01	3	Unchanged	High
Q02878	D01cd1	ribosomal protein L6	15861.7	7300	10119.01	11094.61	6.48E-01	-1.12E+00	3	Unchanged	High
P18124	D03cd1	ribosomal protein L7	21230.67	15900	19538.32	18885.03	-1.20E-01	-4.18E-01	3	Unchanged	High
P11518	G11cd3	ribosomal protein L7a	13385.5	8240	10586.53	10736.39	-3.38E-01	-7.00E-01	3	Unchanged	High
P25120	D05cd1	ribosomal protein L8	23580.43	18300	24766.14	22208.81	7.08E-02	-3.67E-01	3	Unchanged	High
P32969	B19cd1	ribosomal protein L9	28853.42	32200	37288.41	32766.75	3.70E-01	1.56E-01	3	Unchanged	High
P46783	H13cd1	ribosomal protein S10	7453.342	7660	7511.766	7540.695	1.13E-02	3.89E-02	3	Unchanged	High
P04643	H15cd1	ribosomal protein S11	13429.85	15600	13623.52	14209.6	2.07E-02	2.14E-01	3	Unchanged	High
P25398	H17cd1	ribosomal protein S12	16170.73	10600	12294.27	13018.69	-3.95E-01	-6.11E-01	3	Unchanged	High
Q02546	H19cd1	ribosomal protein S13	13956.88	12600	15289.54	13946.74	1.32E-01	-1.48E-01	3	Unchanged	High
P11174	H21cd1	ribosomal protein S15	21322.73	19600	23343.6	21408.92	1.30E-01	-1.24E-01	3	Unchanged	High
P39027	H23cd1	ribosomal protein S15a	16787.1	15100	21854.01	17912.92	3.81E-01	-1.53E-01	3	Unchanged	High
P17008	J01cd1	ribosomal protein S16	26604.5	15700	24481.55	22257.3	-1.20E-01	-7.62E-01	3	Unchanged	High
P08708	J03cd1	ribosomal protein S17	13979.25	7990	15360.88	12443.09	1.36E-01	-8.07E-01	3	Unchanged	High
P25232	A17gh2	ribosomal protein S18	12558.18	12600	20093.07	15089.7	6.78E-01	6.84E-03	3	Unchanged	High
P17075	J07cd1	ribosomal protein S20	21944.13	19900	31381.43	24400.98	5.16E-01	-1.43E-01	3	Unchanged	High
P35265	D24ef7	ribosomal protein S21	14046.7	9470	9023.678	10847.43	-6.38E-01	-5.69E-01	3	Unchanged	High
P39028	J09cd1	ribosomal protein S23	12228.96	10900	14550.17	12545.6	2.51E-01	-1.72E-01	3	Unchanged	High
P16632	J11cd1	ribosomal protein S24	12913.37	13100	12135.49	12699.84	-8.96E-02	1.53E-02	3	Unchanged	High
P25111	J13cd1	ribosomal protein S25	6274.159	5630	5123.747	5677.337	-2.92E-01	-1.55E-01	3	Unchanged	High
P02383	C01cd3	ribosomal protein S26	26138.26	30900	19440.2	25499.92	-4.27E-01	2.42E-01	3	Unchanged	High
P42677	G01cd3	ribosomal protein S27 (metalloph	17556.94	12800	20363.13	16927.4	2.15E-01	-4.51E-01	3	Unchanged	High
P14798	B18cd1	ribosomal protein S27a	3284.651	3180	2757.252	3073.17	-2.52E-01	-4.77E-02	3	Unchanged	High
P25112	J15cd1	ribosomal protein S28	30384.24	32000	28529.21	30318.47	-9.09E-02	7.66E-02	3	Unchanged	High
P30054	J17cd1	ribosomal protein S29	18454.55	20900	25539.27	21630.2	4.69E-01	1.79E-01	3	Unchanged	High
P23396	H03cd1	ribosomal protein S3	5913.682	2830	5523.561	4754.218	-9.85E-02	-1.07E+00	3	Unchanged	High
P49241	O16ef5	ribosomal protein S3A	7154.088	6200	6592.248	7316.667	2.64E-01	-2.06E-01	3	Unchanged	High
P12750	A21cd3	ribosomal protein S4; X-linked	19821.56	16200	21778.05	19282.5	1.36E-01	-2.87E-01	3	Unchanged	High
P22090	A23cd3	ribosomal protein S4; Y-linked	2629.697	2330	2779.184	2580.924	7.98E-02	-1.72E-01	3	Unchanged	High
P46782	H05cd1	ribosomal protein S5	15421.08	11000	17355.54	14598.86	1.70E-01	-4.85E-01	3	Unchanged	High
P10660	H07cd1	ribosomal protein S6	46408.18	26100	40579.46	37695.24	-1.94E-01	-8.30E-01	3	Unchanged	High

P46781	H12cd5	ribosomal protein S9	8827,416	9710	15295.98	11278.36	7.93E-01	1.38E-01	3	Unchanged	High
P46781	P12cd5	ribosomal protein S9	9059,523	1790	5725.082	5525.883	-6.62E-01	-2.34E+00	3	Unchanged	High
P05387	H01cd1	ribosomal protein; large P2	16611.4	12700	17775.72	15695.14	9.78E-02	-3.67E-01	3	Unchanged	High
P05388	F21cd1	ribosomal protein; large; P0	17127,41	12400	19748.88	16430.54	2.05E-01	-4.64E-01	3	Unchanged	High
P05386	F23cd1	ribosomal protein; large; P1	2228,298	1880	3134.529	2413.78	4.92E-01	-2.46E-01	3	Unchanged	High
Q9Y254	C08ef3	ring-box 1	2597,578	4260	3365.165	3408.892	3.74E-01	7.15E-01	3	Unchanged	High
Q9NWJ8	A23gh3	roundabout homolog 4; magic rai	1969,602	3940	2093.279	2666.66	8.79E-02	9.99E-01	3	Unchanged	High
P08206	D06cd1	S100 calcium binding protein A1	38485,73	49800	31745.47	40017.88	-2.78E-01	3.72E-01	3	Unchanged	High
P31949	E09cd3	S100 calcium binding protein A1*	8890,594	11100	5408.269	8466.714	-7.17E-01	3.20E-01	3	Unchanged	High
P06703	P17gh6	S100 calcium binding protein A6	3403,146	4070	2088.478	3188.753	-7.04E-01	2.60E-01	3	Unchanged	High
P55735	J04ef4	SEC13-like 1 (S. cerevisiae)	1695,152	1990	2362.541	2016.062	4.79E-01	2.32E-01	3	Unchanged	High
P38384	I05ef3	Sec61 gamma	5653,955	7820	7254.423	6908.432	3.60E-01	4.67E-01	3	Unchanged	High
Q9NZJ3	H06ef2	selenoprotein T	2923,813	2440	1325.491	2230.091	-1.14E+00	-2.60E-01	3	Unchanged	High
O15532	H16cd1	selenoprotein W; 1	2678,843	2970	3918.44	3189.642	5.49E-01	1.50E-01	3	Unchanged	High
Q13501	J23cd4	sequestosome 1	3214,395	3170	1164.17	2517.543	-1.47E+00	-1.82E-02	3	Unchanged	High
P35237	L18ab8	serine (or cysteine) proteinase In	4203,074	8180	2936.72	5105.477	-5.17E-01	9.60E-01	3	Unchanged	High
P05121	P05ef7	serine (or cysteine) proteinase In	4454,56	7280	9179.863	6972.284	1.04E+00	7.09E-01	3	Unchanged	High
Q00587	C14cd7	serum constituent protein	2480,698	2660	2044.608	2393.46	-2.79E-01	9.80E-02	3	Unchanged	High
Q9H299	P16gh7	SH3 domain binding glutamic acid	14473,6	17100	13798.02	15134.74	-6.90E-02	2.43E-01	3	Unchanged	High
P37108	E21cd2	signal recognition particle 14kD (	24326,27	35600	24319.59	28082.56	-3.96E-04	5.49E-01	3	Unchanged	High
P49458	E19cd2	signal recognition particle 9kD	1874,967	2640	3141.422	2551.928	7.45E-01	4.93E-01	3	Unchanged	High
P43308	G15cd2	signal sequence receptor; beta (I	4209,147	4610	5876.451	4898.581	4.81E-01	1.31E-01	3	Unchanged	High
P51571	O15gh1	signal sequence receptor; delta (	2062,113	2330	2654.968	2349.29	3.65E-01	1.77E-01	3	Unchanged	High
O00422	M17cd6	sin3-associated polypeptide; 18k	2502,79	2610	2079.295	2396.002	-2.67E-01	5.83E-02	3	Unchanged	High
O75918	J10cd5	small EDRK-rich factor 2	5927,595	7010	7926.059	6955.245	4.19E-01	2.42E-01	3	Unchanged	High
P13500	C15cd3	small inducible cytokine A2 (mon	17077,97	38100	8786.323	2130.26	-9.59E-01	1.16E+00	3	Unchanged	High
Q15356	A09cd2	small nuclear ribonucleoprotein p	2743,428	2150	2819.855	2570.901	3.96E-02	-3.52E-01	3	Unchanged	High
P14648	A13cd2	small nuclear ribonucleoprotein p	899,6242	2800	2362.597	2021.429	1.39E+00	1.64E+00	3	Unchanged	High
P12236	G01ef1	solute carrier family 25 (mitochor	7384,066	4760	6176.034	6107.995	-2.58E-01	6.32E-01	3	Unchanged	High
Q00325	K22ab8	solute carrier family 25 (mitochor	5074,308	3750	3779.577	4202.626	-4.25E-01	-4.37E-01	3	Unchanged	High
P32745	N01cd1	somatostatin receptor 3	4102,668	4170	4748.989	4340.964	2.11E-01	2.39E-02	3	Unchanged	High
P30626	E13cd2	sorcin	1895,592	2790	2280.297	2323.149	2.67E-01	5.59E-01	3	Unchanged	High
Q01826	F18ef6	special AT-rich sequence binding	26449,32	41300	24225.61	30645.09	-1.27E-01	6.42E-01	3	Unchanged	High
P21673	D12cd1	sperrmidine/spermine N1-acetyl	8349,882	16500	6013.659	10275.93	-4.74E-01	9.80E-01	3	Unchanged	High
P34991	G05cd3	S-phase kinase-associated protein	3072,601	2990	2396.506	2820.643	-3.59E-01	-3.80E-02	3	Unchanged	High
P23236	B09cd2	splicing factor proline/glutamine I	2694,629	2460	3348.423	2834.056	3.13E-01	-1.32E-01	3	Unchanged	High
P35716	C07cd2	SRY (sex determining region Y)-H	5019,988	4860	2125.089	4001.241	-1.24E+00	-4.71E-02	3	Unchanged	High
P35713	E10ef4	SRY (sex determining region Y)-H	2575,791	3100	2024.386	2565.998	-3.48E-01	2.66E-01	3	Unchanged	High
Q06945	C05cd2	SRY (sex determining region Y)-H	2299,474	2210	1636.067	2049.214	-4.91E-01	-5.59E-02	3	Unchanged	High
P00441	G20ef7	superoxide dismutase 1; soluble	4439,342	4930	3239.195	4202.954	-4.55E-01	1.51E-01	3	Unchanged	High
P50502	H18cd2	suppression of tumorigenicity 13	2307,599	2530	2358.117	2400.085	3.12E-02	1.35E-01	3	Unchanged	High
Q9Y5Y6	P20gh1	suppression of tumorigenicity 14	2358,28	2700	1494.856	2183.041	-6.58E-01	1.93E-01	3	Unchanged	High
P17600	J06cd2	synapsin I	1969,157	2220	2010.908	2067.417	3.03E-02	1.74E-01	3	Unchanged	High
O43759	O02cd2	synaptophysin I	14516,6	10700	1060.61	11775.53	-5.29E-01	-4.33E-01	3	Unchanged	High
Q12962	P19cd2	TAF10 RNA polymerase II; TATA	5937,255	5080	3962.323	4992.528	-5.83E-01	-2.26E-01	3	Unchanged	High
Q15763	B20cd2	t-complex-associated-testis-expn	2022,997	2890	2885.017	2600.459	5.12E-01	5.16E-01	3	Unchanged	High
P10599	B23cd4	thioredoxin	11525,16	11900	6440.37	9965.777	-8.40E-01	5.00E-02	3	Unchanged	High
P13472	O02ef7	thymosin; beta 10	46982,91	74300	54263.48	58508.68	2.08E-01	6.61E-01	3	Unchanged	High
P01253	L12gh1	thymosin; beta 4; X chromosome	23145,54	26000	16231.51	21783.42	-5.12E-01	1.66E-01	3	Unchanged	High
Q01095	O02cd2	TIA1 cytolysin granule-associate	2250,456	1770	2917.342	2312.331	3.74E-01	-3.47E-01	3	Unchanged	High
Q15370	J12cd2	transcription elongation factor B-	2616,595	3980	3919.327	3505.384	5.83E-01	5.60E-01	3	Unchanged	High
O43680	O11cd2	transcription factor 21	1789,295	1790	3044.118	2209.014	7.67E-01	3.49E-03	3	Unchanged	High
P29190	O16cd2	transglutaminase 2 (C polypeptid	3131,079	3490	1857.596	2827.774	-7.53E-01	1.58E-01	3	Unchanged	High
P29401	N15cd1	transkelolase (Wernicke-Korsakoff	3256,575	2040	2715.206	2671.504	-2.63E-01	-6.75E-01	3	Unchanged	High
O60739	O01cd6	translation factor sui1 homolog	2671,935	3400	3868.727	3315.099	5.34E-01	3.50E-01	3	Unchanged	High
Q9NS69	I02gh7	translocase of outer mitochondria	2989,423	2450	3754.914	3062.809	3.29E-01	-2.89E-01	3	Unchanged	High
P00938	M24cd1	triosephosphate isomerase 1	5701,29	5820	8345.738	6622.243	5.50E-01	2.97E-02	3	Unchanged	High
P07226	G10cd2	tropomyosin 4	2636,256	2300	3755.882	2857.509	5.11E-01	-1.97E-01	3	Unchanged	High
P04687	F09cd4	tubulin; alpha 3	20220,03	14500	22303.88	18992.31	1.42E-01	-4.84E-01	3	Unchanged	High
P04687	A01cd1	tubulin; alpha; ubiquitous	15258,81	7840	22478.65	15193.76	5.59E-01	-9.60E-01	3	Unchanged	High
Q13509	E04cd6	tubulin; beta; 4	2338,877	2990	1853.273	2349.885	-3.36E-01	3.56E-01	3	Unchanged	High
P04350	F01gh6	tubulin; beta; 5	7573,765	4430	3448.455	5149.498	-1.14E+00	-7.75E-01	3	Unchanged	High
P75347	O08cd2	tubulin-specific chaperone a	3000,065	3900	3275.629	3390.719	1.27E-01	3.77E-01	3	Unchanged	High
Q75509	L10ef3	tumor necrosis factor receptor su	2245,338	4890	1881.231	3007.078	-2.55E-01	1.12E+00	3	Unchanged	High
P13693	G16cd2	tumor protein; translationally-con	3987,18	60800	4846.285	49731.11	2.81E-01	6.10E-01	3	Unchanged	High
P14625	G24cd2	tumor rejection antigen (gp96) 1	2185,187	2050	4905.342	3049.346	1.17E+00	-8.69E-02	3	Unchanged	High
P42655	K04cd4	tyrosine 3-monooxygenase/trypc	6584,565	5730	5556.974	5956.713	-2.44E-01	-2.01E-01	3	Unchanged	High
Q04917	G06cd3	tyrosine 3-monooxygenase/trypc	6621,322	6150	4562.366	7111.932	-9.18E-01	-8.07E-02	3	Unchanged	High
P29312	A01cd4	tyrosine 3-monooxygenase/trypc	5873,282	4670	2279.148	2745.506	-1.37E+00	-3.29E-01	3	Unchanged	High
P29312	P12cd4	tyrosine 3-monooxygenase/trypc	4562,964	1140	1520.2	2406.497	-1.59E-01	-2.01E+00	3	Unchanged	High
O14957	G17cd7	ubiquinol-cytochrome c reductas	2728,765	3990	3322.422	3351.45	2.88E-01	5.49E-01	3	Unchanged	High
P14793	D01cd4	ubiquitin A-52 residue fbosomal	3536,225	1730	3258.439	2840.732	-1.18E-01	-1.03E+00	3	Unchanged	High
P02248	D22gh1	ubiquitin B	2753,942	4430	4152.235	3779.352	5.92E-01	6.86E-01	3	Unchanged	High
O76069	B12cd4	ubiquitin-conjugating enzyme E2	2001,262	1980	2223.574	2058.646	1.52E-01	-1.46E-02	3	Unchanged	High
Q98ZL1	B17gh7	ubiquitin-like 5	4339,474	9100	5279.835	6239.513	2.83E-01	1.07E+00	3	Unchanged	High
P08670	C24cd3	vimentin	5940,876	6720	17783.4	10813.94	1.58E+00	5.53E-01	3	Unchanged	High
P45880	C18cd3	voltage-dependent anion channel	7005,537	7280	4758.179	6347.014	-5.58E-01	5.49E-02	3	Unchanged	High
Q9Y277	C04cd4	voltage-dependent anion channel	1863,424	2210	2573.885	2216.75	4.66E-01	2.48E-01	3	Unchanged	High
P17861	O15cd4	X-box binding protein 1	3398,455	1600	2040.224	2347.333	-7.36E-01	-1.08E+00	3	Unchanged	High
O43670	M04cd3	zinc finger protein 207	3338,117	3170	3176.631	3226.643	-7.15E-02	-7.67E-02	3	Unchanged	High
Q07352	N21ef6	zinc finger protein 36; C3H type-I	6097,384	5750	4958.224	5601.518	-2.98E-01	-8.49E-02	3	Unchanged	High
Q15942	M10cd3	zyxin	2570,21	2070	2519.748	2387.987	-2.86E-02	-3.09E-01	3	Unchanged	High
Q16659	B17ef5	mitogen-activated protein kinase	144,6425	141	100.0111	128.6073	-5.32E-01	-3.51E-02	1	Unchanged	Low
O75324	B05cd3	stannin	131,7242	172	100.0655	134.7009	-3.97E-01	3.88E-01	1	Unchanged	Low
Q9BYP8	E16gh8	keratin associated protein 17.1	176,4958	174	100.1011	150.0893	-8.18E-01	-2.33E-02</td			

P49768	L14ab7	present in 1 (Alzheimer disease 3)	127.9653	124	100.3504	117.5823	-3.51E-01	-4.04E-02	1	Unchanged	Low
P55107	G10ab5	growth differentiation factor 10	114.7206	168	100.6326	127.9343	-1.89E-01	5.54E-01	1	Unchanged	Low
P17082	P18cd7	related RAS viral (r-ras) oncogene	433.219	176	100.8465	236.7778	-2.10E+00	-1.30E+00	1	Unchanged	Low
P23634	N08ab2	ATPase; Cat++ transporting; plus	179.3836	276	100.9041	185.4081	-8.30E-01	6.21E-01	1	Unchanged	Low
P78347	J20ab5	general transcription factor II; I	151.6834	103	100.9514	118.6963	-5.87E-01	-5.52E-01	1	Unchanged	Low
P09912	F08ef7	interferon: alpha-inducible protein	183.6419	1050	101.0749	444.3716	-8.61E-01	2.51E+00	1	Unchanged	Low
Q9H2F5	F13gh7	enhancer of polycomb 1	127.3938	115	101.3763	114.5773	-3.30E-01	-1.48E-01	1	Unchanged	Low
O14811	M06cd7	programmed cell death 10	152.3457	132	101.5956	128.8019	-6.85E-01	-2.02E-01	1	Unchanged	Low
O60942	A17cd4	RNA guanylyltransferase and 5'-	176.7836	97.1	101.6765	125.1735	-7.98E-01	-8.65E-01	1	Unchanged	Low
Q9V5Y3	M18cd7	G protein-coupled receptor 45	174.3335	161	101.8478	145.8355	-7.75E-01	-1.12E-01	1	Unchanged	Low
P11908	H15ab8	phosphotbosy pyrophosphate s:	166.1373	174	101.9334	147.2722	-7.05E-01	6.46E-02	1	Unchanged	Low
Q92851	P18ab3	caspase 10; apoptosis-related cy	135.919	107	101.9435	115.0308	-4.15E-01	-3.42E-01	1	Unchanged	Low
Q9BQE5	M03gh7	apolipoprotein L; 2	109.8196	148	102.0533	119.8218	-1.06E-01	4.26E-01	1	Unchanged	Low
P55327	D05cd2	tumor protein D52	136.2596	112	102.1111	116.9522	-4.16E-01	-2.77E-01	1	Unchanged	Low
P28332	K03ab2	alcohol dehydrogenase 6 (class 1)	142.4055	97.7	102.1575	114.0924	-4.79E-01	-5.43E-01	1	Unchanged	Low
O59861	E02cd8	3'(2'); 5'-bisphosphate nucleotida	161.1251	116	102.1715	115.4153	-3.27E-01	-1.44E-01	1	Unchanged	Low
Q9NXJ5	A10gh2	hypothetical protein FLJ20208	122.4219	151	102.3030	125.3222	-2.59E-01	3.05E-01	1	Unchanged	Low
Q15842	K09gh1	thyroid hormone receptor Interac	120.9158	142	102.3082	121.6641	-2.41E-01	2.30E-01	1	Unchanged	Low
O94997	O09cd7	decidua protein Induced by prog	174.3087	140	102.3137	138.8592	-7.69E-01	-3.17E-01	1	Unchanged	Low
O95453	G02ab8	poly(A)-specific ribonuclease (d)	139.9344	105	102.3217	115.7147	-4.52E-01	-4.16E-01	1	Unchanged	Low
Q9H9C5	F01gh7	KIAA1453 protein	135.8299	126	102.4347	121.5247	-4.07E-01	-1.05E-01	1	Unchanged	Low
P10451	B13cd1	secreted phosphoprotein 1 (oste	190.4604	76.7	102.5193	123.2388	-8.94E-01	-1.31E+00	1	Unchanged	Low
P53992	B03cd5	SEC24 related gene family; mem	134.307	105	102.5437	113.9998	-3.89E-01	-3.53E-01	1	Unchanged	Low
Q9NQW1	F22gh6	secretory pathway component St	111.3643	158	102.6234	123.8833	-1.18E-01	5.02E-01	1	Unchanged	Low
Q01449	A17gh5	myosin light chain 2a	179.1031	170	103.0725	150.5611	-7.97E-01	-7.94E-02	1	Unchanged	Low
Q9NQX46	K12gh2	hypothetical protein FLJ20446	109.5374	159	103.1083	123.8664	-8.73E-02	5.37E-01	1	Unchanged	Low
P53609	A23cd1	protein geranylgeranyltransferases	140.0296	128	103.1248	123.8135	-4.41E-01	-1.26E-01	1	Unchanged	Low
Q15029	J16cd4	U5 snRNP-specific protein; 116	119.3284	126	103.1503	115.9932	-2.10E-01	7.28E-02	1	Unchanged	Low
P50458	O23cd5	LIM homeobox protein 2	145.905	120	103.1971	122.9669	-5.00E-01	-2.84E-01	1	Unchanged	Low
P33764	B24cd1	S100 calcium binding protein A3	150.5991	204	103.3783	152.5858	-5.43E-01	4.36E-01	1	Unchanged	Low
Q9P289	G03ef3	Mst3 and SOX1-related kinase	133.5225	116	103.4345	117.7841	-3.68E-01	-1.98E-01	1	Unchanged	Low
P52429	P17cd5	dihydrocerol kinase; epsilon (d)	128.7238	123	103.5015	118.2956	-3.15E-01	-6.96E-02	1	Unchanged	Low
P54578	H17cd5	ubiquitin specific protease 14 (IR	160.7495	108	103.6684	124.2132	-6.33E-01	-5.71E-01	1	Unchanged	Low
Q13219	E24ab8	pregnancy-associated plasma pr	112.9052	154	103.7948	123.4254	-1.21E-01	4.44E-01	1	Unchanged	Low
O60547	M12ab7	GDP-mannose 4,6-dehydratase	147.2805	108	103.8004	119.8044	-5.05E-01	-4.43E-01	1	Unchanged	Low
P23297	H17ef6	S100 calcium binding protein A1	145.2558	126	103.9033	124.9008	-4.83E-01	-2.10E-01	1	Unchanged	Low
Q9HJS8	M01gh6	hypothetical protein MGC5306	216.0991	91.7	104.0432	137.2762	-1.05E+00	-1.24E+00	1	Unchanged	Low
Q14493	I08cd4	stem-loop (histone) binding prole	126.7755	155	104.1318	128.4702	-2.84E-01	2.85E-01	1	Unchanged	Low
Q9NZU0	K16cd8	fibronectin leucine rich transmem	284.9107	268	104.3033	219.1816	-1.45E+00	-8.65E-02	1	Unchanged	Low
P80370	B01ef7	delta-like 1 homolog (Drosophila)	160.1421	80	104.3226	114.8185	-6.18E-01	-1.00E+00	1	Unchanged	Low
Q9NYV4	C23ef3	CDC2-related protein kinase 7	128.5947	107	104.3521	113.4542	-3.01E-01	-2.80E-01	1	Unchanged	Low
P09016	C23ef5	homeo box D4	173.2254	192	104.3556	156.5829	-7.31E-01	1.50E-01	1	Unchanged	Low
Q13873	A16ab3	bone morphogenetic protein rece	155.8113	86.8	104.4206	115.6624	-5.77E-01	-8.45E-01	1	Unchanged	Low
Q14878	B22ef4	Inosine triphosphatase (nucleosid	124.8814	120	104.4238	116.3938	-2.58E-01	-5.89E-02	1	Unchanged	Low
P52848	J01ab5	N-deacetylase/N-sulfotransf erase	165.2411	84.4	104.4555	118.3793	-6.70E-01	-9.77E-01	1	Unchanged	Low
Q14848	A05cd5	TNF receptor-associated factor 4	124.2461	136	104.4604	121.4689	-2.50E-01	1.27E-01	1	Unchanged	Low
O00204	O04cd2	sulfotransferase family; cytosolic	185.8106	117	104.4824	135.6533	-8.31E-01	-6.71E-01	1	Unchanged	Low
P35610	E13gh1	sterol O-acyltransferase (acyl-Cc	143.8417	88	104.5518	112.1404	-4.60E-01	-7.08E-01	1	Unchanged	Low
Q04760	L03ab5	glyoxalase I	132.6871	107	104.5782	114.7132	-3.43E-01	-3.12E-01	1	Unchanged	Low
P51690	H06ab2	arylsulfatase E (chondrodysplasi	177.023	76.2	104.5865	119.2772	-7.59E-01	-1.22E+00	1	Unchanged	Low
P26012	C11ef7	integrin; beta 8	110.7396	170	104.5295	128.4899	-8.19E-02	6.19E-01	1	Unchanged	Low
Q14978	K11cd5	nucleolar and coiled-body phosph	117.0048	131	104.685	117.4911	-1.61E-01	1.61E-01	1	Unchanged	Low
O00764	D16cd3	pyridoxal (pyridoxine; vitamin B6	160.2678	140	104.6915	135.073	-6.14E-01	-1.92E-01	1	Unchanged	Low
Q9Y6Q5	P13cd5	adaptor-related protein complex	149.3929	107	104.7705	120.3004	-5.12E-01	-4.85E-01	1	Unchanged	Low
O95350	G04cd5	Homer; neuronal Immediate early	137.2833	126	104.7829	122.6314	-3.90E-01	-1.26E-01	1	Unchanged	Low
P49748	C13ab2	acyl-Coenzyme A dehydrogenas	121.151	141	104.7897	122.4441	-2.09E-01	2.23E-01	1	Unchanged	Low
P08100	O24cd1	rhodopsin (opsin 2; rod pigment)	125.5282	116	104.8101	115.4338	-2.58E-01	-1.10E-01	1	Unchanged	Low
Q15477	F24cd2	superkiller viralicidic activity 2-like	102.5551	186	104.8138	131.0636	-3.14E-02	8.58E-01	1	Unchanged	Low
O43520	H17cd1	ATPase; Class I; type BB; memb	199.1157	91.5	104.8252	131.8072	-9.26E-01	-1.12E+00	1	Unchanged	Low
Q13039	P02ef4	ATP-binding cassette; sub-family	175.7841	80.5	104.8585	120.383	-7.45E-01	-1.13E+00	1	Unchanged	Low
O15291	L12cd1	solute carrier family 7 (cationic a	276.3689	176	104.904	185.7368	-1.40E+00	-6.52E-01	1	Unchanged	Low
Q9NR71	L23gh4	mitochondrial ceramidase	108.9644	152	104.9361	122.0931	-5.43E-02	4.84E-01	1	Unchanged	Low
O60884	H10cd4	DnaJ (Hsp40) homolog; subfamily	221.9835	239	104.9441	168.5763	-1.08E+00	1.05E-01	1	Unchanged	Low
Q9BYE0	J17gh8	hairy and enhancer of split 7 (Drt	128.0255	108	104.9542	113.8134	-2.87E-01	-2.39E-01	1	Unchanged	Low
Q9Y272	L01ef2	RAS; dexamethasone-induced 1	101.2051	166	104.9825	124.0354	-5.29E-02	7.13E-01	1	Unchanged	Low
Q9BUR5	M13gh6	hypothetical protein MGC4825	78.2636	239	105.0137	140.65	-4.24E-01	1.61E+00	1	Unchanged	Low
O60859	A13cd7	neuropathy target esterase	123.9707	117	105.029	115.3513	-2.39E-01	-8.28E-02	1	Unchanged	Low
Q9GZU1	A20gh4	mucolipin 1	85.32301	243	105.1039	144.4516	-3.01E-01	1.51E+00	1	Unchanged	Low
P19878	B15ab6	neutrophil cytosolic factor 2 (65k	310.5103	515	105.1041	310.3051	-1.56E+00	7.31E-01	1	Unchanged	Low
Q13277	K12cd2	synlaxin 3A	118.5375	165	105.2511	136.1937	-1.72E-01	6.41E-01	1	Unchanged	Low
	B04gh8	reserved	130.849	124	105.2594	120.0361	-3.14E-01	-7.76E-02	1	Unchanged	Low
P32456	N18ab4	guanylate binding protein 2; Inter	109.3786	142	105.2611	118.8515	-5.54E-02	3.76E-01	1	Unchanged	Low
Q9H4M9	E01cd7	EH-domain containing 1	149.0051	151	105.3893	134.9992	-5.00E-01	1.54E-02	1	Unchanged	Low
Q9BTX7	O19gh6	chromosome 20 open reading fra	115.9099	157	105.4128	126.2023	-1.37E-01	4.40E-01	1	Unchanged	Low
Q9NVN2	M02gh3	solute carrier family 4 (anion exd	123.8178	114	105.466	114.476	-2.31E-01	-1.17E-01	1	Unchanged	Low
Q99758	A17ab2	ATP-binding cassette; sub-family	238.456	145	105.5504	163.1362	-1.18E+00	-7.14E-01	1	Unchanged	Low
P43694	B06ef6	GATA binding protein 4	107.7539	161	105.5891	124.6996	-2.93E-02	5.77E-01	1	Unchanged	Low
Q13825	C07eb3	AU RNA binding protein/enoyl-Cc	123.4494	140	105.5872	123.0884	-2.25E-01	1.83E-01	1	Unchanged	Low
Q92550	L23ef3	ring finger protein 10	197.4603	112	105.7052	138.2365	-9.02E-01	-8.24E-01	1	Unchanged	Low
Q9UJS0	C12ef3	solute carrier family 25; member	119.1806	139	105.8216	121.1782	-1.72E-01	2.17E-01	1	Unchanged	Low
Q99611	O05ef3	selenophosphate synthetase 2	168.8742	128	105.8955	134.292	-6.73E-01	-3.99E-01	1	Unchanged	Low
P17275	F08ab6	jun B proto-oncogene	135.9478	94.9	105.9141	112.2701	-3.60E-01	-5.18E-01	1	Unchanged	Low
Q13477	Rn9cd4	mucosal vascular addressin cell	127.8352	110	105.9239	114.7415	-2.71E-01	-2.11E-01	1	Unchanged	Low

P50991	H09cd6	chaperonin containing TCP1; sut	161.4396	148	106.0337	138.5513	-6.06E-01	-1.23E-01	1	Unchanged Low
P35548	K11ab7	msh homeo box homolog 2 (Dros	182.4309	124	107.5011	137.5011	-7.63E-01	-5.57E-01	1	Unchanged Low
P11309	M14ab8	plm-1 oncogene	136.3951	99	106.0757	113.8227	-3.63E-01	-4.62E-01	1	Unchanged Low
O75570	A03cd5	mitochondrial translational releas	128.9238	118	106.1208	117.597	-2.81E-01	-1.31E-01	1	Unchanged Low
Q9NY61	O01ef3	apoptosis antagonizing transcript	120.3605	124	106.1404	116.8527	-1.81E-01	4.36E-02	1	Unchanged Low
Q9BTY8	D01gh7	hypothetical protein MGC4342	139.5304	92.9	106.2168	112.876	-3.94E-01	-5.87E-01	1	Unchanged Low
Q9NWS2	F09gh2	hypothetical protein FLJ20640	183.0823	140	106.2384	143.0354	-7.85E-01	-3.89E-01	1	Unchanged Low
O00180	H06ab6	potassium channel; subfamily K;	129.4915	122	106.2703	119.3824	-2.85E-01	-8.14E-02	1	Unchanged Low
O15382	I05ab3	branched chain aminotransferase	136.8391	95.5	106.3058	112.8868	-3.64E-01	-5.19E-01	1	Unchanged Low
Q9Y2Z1	D05ef2	CGI-01 protein	156.4563	198	106.3369	153.067	-3.75E-01	3.28E-01	1	Unchanged Low
Q9Y315	E18ef2	CGI-26 protein	135.7793	111	106.6662	117.8557	-3.48E-01	-2.89E-01	1	Unchanged Low
Q9Y592	P20ef1	NY-REN-58 antigen	118.6541	121	106.7049	115.3792	-1.53E-01	2.56E-02	1	Unchanged Low
Q9NYT0	D20ef3	pleckstrin 2 (mouse) homolog	114.999	153	106.7508	124.8364	-1.07E-01	4.10E-01	1	Unchanged Low
Q9Y343	M10ef4	SBB131 protein	123.0625	120	106.8362	116.6438	-2.04E-01	-3.60E-02	1	Unchanged Low
Q9BV4	G09gh6	hypothetical protein MGC3162	140.5988	123	106.8523	123.6298	-3.96E-01	-1.88E-01	1	Unchanged Low
P30622	B20cd1	restin (Reed-Stenberg cell-expres	116.8074	136	107.0013	119.7985	-1.27E-01	2.15E-01	1	Unchanged Low
Q08345	F08ef5	discoidin domain receptor family:	266.6468	264	107.136	212.6497	-1.32E-01	-1.35E-02	1	Unchanged Low
P33176	C16ab7	kinesin family member 5B	123.5679	113	107.2314	114.5075	-2.05E-01	-1.33E-01	1	Unchanged Low
P55273	D14ab4	cyclin-dependent kinase inhibitor	99.64375	174	107.4234	126.8971	-1.08E-01	8.01E-01	1	Unchanged Low
Q9NW92	E10gh3	hypothetical protein FLJ10209	177.1237	166	107.454	150.3287	-7.21E-01	-9.00E-02	1	Unchanged Low
Q9NZC3	K03ef3	membrane interacting protein of I	105.8303	152	107.465	121.8015	-2.21E-01	5.23E-01	1	Unchanged Low
P15172	M19ab7	myogenic factor 3	132.7839	110	107.4694	116.7347	-3.05E-01	-2.72E-01	1	Unchanged Low
P27144	A06ab2	adenylyl kinase 3	118.5733	124	107.598	116.7128	-1.40E-01	6.42E-02	1	Unchanged Low
O60508	A08ef2	pre-mRNA splicing factor 17	150.1968	130	107.6187	129.259	-4.81E-01	-2.09E-01	1	Unchanged Low
Q14012	B08cd3	calcium/calmodulin-dependent pi	113.9231	135	107.6204	118.8965	-8.21E-02	2.46E-01	1	Unchanged Low
P98179	G12cd1	RNA binding motif protein 3	140.1356	93.2	107.7553	113.6891	-3.79E-01	-5.89E-01	1	Unchanged Low
Q13223	E10ab2	BRF1 homolog; subunit of RNA p	150.0469	115	107.7567	124.3969	-4.76E-01	-3.79E-01	1	Unchanged Low
P55198	N09ab7	myeloid/lymphoid or mixed-linea	180.7113	122	107.7762	136.7768	-7.46E-01	-5.69E-01	1	Unchanged Low
P46459	G02ef1	N-ethylmaleimide-sensitive factor	138.9363	95.7	107.8044	114.1635	-3.66E-01	-5.37E-01	1	Unchanged Low
P34969	I21ef1	S-hydroxytryptamine (serotonin)	218.7666	161	107.8181	169.3507	-1.02E+00	-2.70E-01	1	Unchanged Low
Q14667	K02gh1	KIAA0100 gene product	105.9471	222	107.8612	145.1883	-2.58E-02	1.07E+00	1	Unchanged Low
Q92830	J14cd8	GCN5 general control of amino-e	129.4527	106	107.863	114.5758	-2.63E-01	-2.83E-01	1	Unchanged Low
P14cd2	RNA binding motif protein; Y chr	112.3917	153	107.9125	124.4395	-5.87E-02	4.45E-01	1	Unchanged Low	
O43252	J01cd5	3'-phosphoadenosine 5'-phosph	194.4946	188	107.9154	163.4169	-8.50E-01	-5.02E-02	1	Unchanged Low
Q9NS93	G09ef3	seven transmembrane protein TM	138.0932	237	107.9483	160.8518	-3.55E-01	7.76E-01	1	Unchanged Low
O60616	E20ab6	core-binding factor; runt domain;	489.0924	48.1	107.9963	215.0608	-2.18E+00	-3.35E+00	1	Unchanged Low
P02261	D19cd4	H2A histone family; member C	145.0821	84.1	108.023	112.4051	-4.26E-01	-7.87E-01	1	Unchanged Low
Q14701	F18ef7	DNA cross-link repair 1A (PSO2	119.2486	307	108.208	178.2467	-1.40E-01	1.37E-00	1	Unchanged Low
Q9P025	A04ef8	HSPC135 protein	160.3109	135	108.2493	134.6437	-5.67E-01	-2.44E-01	1	Unchanged Low
P06702	O12ef7	S100 calcium binding protein A9	144.7319	163	108.2576	138.5985	-4.19E-01	1.70E-01	1	Unchanged Low
Q9Y5Q9	P05cd7	general transcription factor IIIC; I	138.644	220	108.3524	155.7377	-3.56E-01	6.68E-01	1	Unchanged Low
P19075	O20cd2	transmembrane 4 superfamily mt	129.5468	103	108.6355	113.7491	-2.54E-01	-3.30E-01	1	Unchanged Low
O60905	B16cd4	sperm associated antigen 9	110.7683	139	108.6913	119.4574	-2.73E-02	3.27E-01	1	Unchanged Low
Q13322	F24ef5	growth factor receptor-bound pro	120.8593	115	108.7182	114.7351	-1.53E-01	-7.64E-02	1	Unchanged Low
Q9UQ09	L01gh1	KIAA0470 gene product	190.3667	103	108.9005	134.0152	-8.05E-01	-8.89E-01	1	Unchanged Low
P57053	J20gh6	H2B histone family; member S	113.6057	199	108.9238	140.5964	-6.07E-02	8.11E-01	1	Unchanged Low
Q92876	J03ab8	kalikrein 6 (neurokin; zyme)	197.2979	130	108.9303	145.5667	-8.57E-01	-5.97E-01	1	Unchanged Low
P09960	F21ab6	leukotriene A4 hydrolase	96.36818	185	109.0526	130.2822	-1.78E-01	9.44E-01	1	Unchanged Low
Q9HBH1	O02gh5	peptide deformylase-like protein	138.0653	91	109.0612	112.7249	-3.40E-01	-6.01E-01	1	Unchanged Low
P55082	L15ab7	microfibrillar-associated protein 3	121.4467	124	109.134	118.1545	-1.54E-01	2.87E-02	1	Unchanged Low
Q9NV6	B01gh3	trinucleosylidine hydroxylase; eps	174.7559	81.6	109.1442	121.828	-6.79E-01	-1.10E+00	1	Unchanged Low
O95249	K10cd5	golgi SNAP receptor complex me	107.5878	143	109.1657	119.983	-2.10E-02	4.12E-01	1	Unchanged Low
Q13891	M15ab6	basic transcription factor 3; like 2	126.6543	120	109.1942	118.5076	-2.14E-01	-8.18E-02	1	Unchanged Low
Q9BZM5	H05gh7	UL16 binding protein 2	133.6731	245	109.2193	162.5485	-2.91E-01	8.73E-01	1	Unchanged Low
O94913	O20ef2	PCF11p homolog	205.6752	80.3	109.2409	131.7517	-9.13E-01	-1.36E+00	1	Unchanged Low
Q12987	E03ef4	acidic 82 kDa protein mRNA	132.1136	117	109.4318	119.3623	-2.72E-02	-1.81E-01	1	Unchanged Low
Q92499	D05ab5	DEAD/H (Asp-Glu-Ala-Asp/His)t	176.6983	124	109.4356	136.6656	-6.91E-01	-5.13E-01	1	Unchanged Low
Q13686	B19ab2	alkylation repair; alkB homolog	105.5169	143	109.4797	119.4385	-5.32E-02	4.42E-01	1	Unchanged Low
P43250	I08ab4	G protein-coupled receptor kinas	120.3579	113	109.4844	114.2814	-1.37E-01	-9.10E-02	1	Unchanged Low
Q9UMX0	L03ef4	ubiquitin 1	122.0111	141	109.5522	124.0398	-1.55E-01	2.04E-01	1	Unchanged Low
Q94905	G12cd7	chromosome 8 open reading frar	127.8659	107	109.6202	114.8261	-2.22E-01	-2.57E-01	1	Unchanged Low
Q9UHK0	K01cd8	nuclear fragile X mental retardat	157.4757	87.6	109.6296	118.2396	-5.22E-01	-8.46E-01	1	Unchanged Low
P25189	D01ab6	myelin protein zero (Charcot-Mar	110.5502	132	109.6859	117.3068	-1.13E-02	2.52E-01	1	Unchanged Low
Q10567	M11ab2	adaptor-related protein complex	208.9283	187	109.8204	168.4738	-9.28E-01	-1.62E-01	1	Unchanged Low
O15230	D18cd8	laminin; alpha 5	111.864	141	109.8469	120.9363	-2.63E-02	3.35E-01	1	Unchanged Low
P52294	J10ab6	karyopherin alpha 1 (importin alp	178.7513	169	109.9831	152.7331	-7.01E-01	-7.70E-02	1	Unchanged Low
O60668	M03cd2	TAF2 RNA polymerase II; TATA	123.6244	111	110.0571	114.8794	-1.68E-01	-1.56E-01	1	Unchanged Low
P11686	J02cd1	surfactant; pulmonary-associated	136.0267	117	110.0847	121.0017	-3.05E-01	-2.19E-01	1	Unchanged Low
Q9NW86	P03gh2	hypothetical protein FLJ10154	174.7789	75	110.1306	119.9579	-6.66E-01	-1.22E+00	1	Unchanged Low
Q9H028	E22gh8	histone deacetylase 10	107.5034	138	110.1585	118.4626	-3.52E-02	3.57E-01	1	Unchanged Low
Q9UJM22	O22cd7	AP1 gamma subunit binding prot	120.2821	119	110.2219	116.5628	-1.26E-01	-1.32E-02	1	Unchanged Low
P24752	C15ab2	acetyl-Coenzyme A acetyltransfer	216.1409	114	110.2562	146.8035	-9.71E-01	-9.23E-01	1	Unchanged Low
P11230	B06ab3	cholinergic receptor; nicotinic; b	106.1774	151	110.2999	122.607	-5.50E-02	5.11E-01	1	Unchanged Low
O14977	O18ef2	ornithine decarboxylase antizym	119.9172	129	110.3	119.7626	-1.21E-01	1.06E-01	1	Unchanged Low
P56937	E15ef5	T cell receptor beta locus	139.7091	844	110.3287	364.6946	-3.41E-01	2.59E+00	1	Unchanged Low
Q99933	E02ef6	hydroxysteroid (17-beta) dehydr	227.1137	74.5	110.3428	137.3284	-1.04E+00	-1.61E+00	1	Unchanged Low
O75299	B21ab7	kinesin family member C3	113.15	128	110.3535	117.1803	-3.61E-02	1.78E-01	1	Unchanged Low
P16219	C09ab2	acyl-Coenzyme A dehydrogenas	109.4688	136	110.3636	118.69	-1.17E-02	3.16E-01	1	Unchanged Low
Q9NZ48	J20gh3	uncharacterized hematopoietic st	112.5665	189	110.3995	137.2614	-2.80E-02	7.46E-01	1	Unchanged Low
Q9P163	L10gh4	hypothetical protein PRO2521	101.1317	159	110.4184	123.4514	-1.27E-01	6.51E-01	1	Unchanged Low
Q9BVT8	I07gh8	hypothetical protein MGC5442	135.5302	137	110.5044	127.7419	-2.95E-01	1.76E-02	1	Unchanged Low
Q99933	E02ef6	BCL2-associated athanogene	119.7332	115	110.533	115.0469	-1.15E-01	-5.98E-02	1	Unchanged Low
O14645	M12cd3	dynlin; exonemal; light Intermedi	164.1806	207	110.5493	160.4204	-5.71E-01	3.31E-01	1	Unchanged Low
Q98RR9	E01gh8	Rho GTPase activating protein 9	120.3646	115	110.5606	115.1711	-1.23E-01	-7.10E-02	1	Unchanged Low
Q9Y3E7	J19ef2	CGI-149 protein	158.4397	202	110.6074	157.1807	-5.18E-01	3.54E-01	1	Unchanged Low
P46976	C09ab6	glycogenin	127.6502	117	110.6815	118.5706	-2.06E-01	-1.21E-01	1	Unchanged Low

O75928	C01cd5	Protein inhibitor of activated STA	98.84393	173	110.7286	127.4786	1.64E-01	8.06E-01	1 Unchanged Low
Q9NX63	I18gh2	hypothetical protein FLJ20420	123.3725	159	110.8068	131.148	-1.55E-01	3.68E-01	1 Unchanged Low
Q9UBS0	I20cd2	ribosomal protein S6 kinase; 70k	186.953	155	110.8188	150.9199	-7.54E-01	-2.71E-01	1 Unchanged Low
Q15185	F18cd5	inactive progesterone receptor;	169.4269	72.3	110.8534	117.54	-6.12E-01	-1.23E+00	1 Unchanged Low
D60516	J18cd3	eukaryotic translation Initiation factor 104.3739	104.3739	147	110.9085	120.8526	8.76E-02	4.97E-01	1 Unchanged Low
Q16651	J01ab8	protease; serine; 8 (prostasin)	334.0498	125	110.9253	190.1399	-1.59E+00	-1.41E+00	1 Unchanged Low
P48788	E22cd2	troponin I; skeletal; fast	121.3602	110	110.9357	114.1376	-1.30E-01	-1.40E-01	1 Unchanged Low
Q01968	N06ab7	oculocerebrorenal syndrome of L	169.0079	95.9	110.9507	125.3025	-6.07E-01	-8.17E-01	1 Unchanged Low
Q9H6Z6	L11gh7	hypothetical protein FLJ21628	115.1546	126	111.0337	117.2667	-5.26E-02	1.25E-01	1 Unchanged Low
Q9NQ55	B01gh4	peter pan homolog (Drosophila)	122.449	120	111.0627	117.676	-1.41E-01	-3.50E-02	1 Unchanged Low
D95359	A24gh1	transforming; acidic coiled-coil $\alpha$	108.2194	139	111.0999	119.4624	3.79E-02	3.62E-01	1 Unchanged Low
P01189	H15ab8	proopiomelanocortin (adrenocort	145.0634	90.4	111.1389	115.5442	-3.84E-01	-6.82E-01	1 Unchanged Low
Q9Y525	G13cd8	v-maf musculoaponeurotic fibros:	119.023	141	111.1934	123.6546	-9.82E-02	2.42E-01	1 Unchanged Low
Q9UHC9	L09cd8	NPC1 (Niemann-Pick disease; type	107.7403	138	111.3741	118.9021	4.79E-02	3.53E-01	1 Unchanged Low
Q9HB72	P14gh7	hypothetical protein PP1057	147.5097	98	111.4385	118.9743	-4.05E-01	-5.90E-01	1 Unchanged Low
D00219	M22ef1	hyaluronan synthase 3	224.5087	89	111.4539	141.641	-1.01E+00	-1.34E+00	1 Unchanged Low
P22735	M16cd1	transglutaminase 1 (K polypeptid	136.8808	91	111.5589	113.1407	-2.95E-01	-5.89E-01	1 Unchanged Low
D15388	A11ab4	slamic acid binding Ig-like lectin 6	105.2847	147	111.6016	121.3043	8.41E-02	4.82E-01	1 Unchanged Low
D95389	J01cd4	WNT1 Inducible signalling pathway	134.8825	94	111.6123	113.4959	-2.73E-01	-5.21E-01	1 Unchanged Low
Q06190	D21ab8	protein phosphatase 2 (formerly)	134.6973	102	111.8192	116.2494	-2.69E-01	-3.98E-01	1 Unchanged Low
P50226	C03cd3	sulfotransferase family; cytosolic	147.6874	101	111.8328	120.0792	-4.01E-01	-5.52E-01	1 Unchanged Low
Q16632	N10ab5	general transcription factor IIIC; I	120.7982	116	111.85	116.1383	-1.11E-01	-6.14E-02	1 Unchanged Low
P54762	A24ef7	EphB1	107.3397	168	111.8869	129.1191	5.96E-02	6.48E-01	1 Unchanged Low
Q15269	E15cd1	PWP2 pericardial tryptophan protei	125.0568	107	111.8713	114.654	-1.61E-01	-2.25E-01	1 Unchanged Low
O14495	H10cd3	phosphatidyl acid phosphatase h	120.761	109	111.9087	113.9808	-1.10E-01	-1.44E-01	1 Unchanged Low
Q9P0U0	N24ef3	PC326 protein	152.5639	101	111.9543	121.9267	-4.47E-01	-5.91E-01	1 Unchanged Low
P50120	J02ab5	retinol binding protein 2; cellular	231.806	217	111.9539	187.0028	-1.05E+00	-9.36E-02	1 Unchanged Low
Q9UH-R0	D08gh1	G protein-coupled receptor kinas	111.83	151	111.9778	124.9147	1.91E-03	4.33E-01	1 Unchanged Low
Q13977	A12ef1	cerebellar degeneration-related 1	105.2052	180	112.0477	132.4319	9.09E-02	7.75E-01	1 Unchanged Low
P51692	C18cd8	signal transducer and activator o	126.7779	100	112.0645	112.9412	-1.78E-01	-3.43E-01	1 Unchanged Low
P51164	N12ab2	ATPase; H $^{+}$ /K $^{+}$ exchanging; bet	136.4695	112	112.2007	120.3347	-2.82E-01	-2.81E-01	1 Unchanged Low
Q9NXH3	C02gh2	protein phosphatase 1; regulator	113.3081	127	112.2521	117.6836	-1.35E-02	1.70E-01	1 Unchanged Low
Q04947	J06ab7	ER to nucleus signalling 2	112.9203	125	112.2701	116.8558	-8.33E-03	1.51E-01	1 Unchanged Low
P16435	G16ef6	P450 (cytochrome) oxdoreducta	110.2003	132	112.2899	118.227	2.71E-02	2.62E-01	1 Unchanged Low
E05gh6		hypothetical protein MGC5338	116.1511	137	112.3522	121.7814	-4.80E-02	2.36E-01	1 Unchanged Low
Q02080	L03ab7	MADS box transcription enhance	138.6124	100	112.3745	117.0502	-3.03E-01	-4.69E-01	1 Unchanged Low
Q15334	J06ab7	lethal giant larvae homolog 1 (Dr	123.3076	110	112.3993	115.3049	-1.34E-01	-1.62E-01	1 Unchanged Low
P10636	J13ab7	microtubule-associated protein t	158.8818	142	112.4092	123.46	-4.39E-02	2.94E-01	1 Unchanged Low
Q9Y4J6	A01gh2	zinc finger protein 6 (CMPX1)	138.8767	102	112.4376	117.8247	-3.05E-01	-4.43E-01	1 Unchanged Low
Q9UHY7	P18gh4	E-1 enzyme	108.9217	134	112.5485	118.5336	4.73E-02	3.00E-01	1 Unchanged Low
Q14147	K04gh1	DEAD/H (Asp-Glu-Ala-Asp/His) t	117.5358	119	112.7866	116.4348	-5.95E-02	1.76E-02	1 Unchanged Low
Q95880	N06gh4	KIAA1513 protein	168.2097	104	112.9115	128.5046	-5.75E-01	-6.88E-01	1 Unchanged Low
Q15013	J23ef3	gene predicted from cDNA with a	104.556	198	113.0807	138.5918	1.13E-01	9.22E-01	1 Unchanged Low
Q9P1E2	E01gh4	hypothetical protein PRO2219	138.6039	107	113.1066	119.6868	-2.93E-01	-3.69E-01	1 Unchanged Low
P07203	H23ef1	glutathione peroxidase 1	120.5127	114	113.1788	115.8519	-9.06E-02	-8.19E-02	1 Unchanged Low
Q13206	M07ab5	DEAD/H (Asp-Glu-Ala-Asp/His) t	140.5274	92.5	113.1804	115.4153	-3.12E-01	-6.03E-01	1 Unchanged Low
O15085	L15ef3	Rho guanine nucleotide exchang	121.8405	111	113.2492	115.3055	-1.05E-01	-1.37E-01	1 Unchanged Low
P48426	C07cd1	phosphatidylinositol 4-phosphate	232.9191	163	113.2533	169.6778	-1.04E+00	-5.16E-01	1 Unchanged Low
Q9NRQ2	K20gh4	phospholipid scramblase 4	126.2397	116	113.2849	118.4782	-1.56E-01	-1.23E-01	1 Unchanged Low
O43171	B24cd3	CDC14 cell division cycle 14 hor	126.784	113	113.382	117.8862	-1.61E-01	-1.60E-01	1 Unchanged Low
Q9HB90	M02gh5	Rag C protein	132.9037	136	113.4299	127.5656	-2.29E-01	3.71E-02	1 Unchanged Low
Q9H733	I21gh5	single Ig IL-1R-related molecule	113.5449	137	113.4753	121.334	-8.84E-04	2.71E-01	1 Unchanged Low
P43353	C06ab2	aldehyde dehydrogenase 3 famil	141.7651	101	113.5244	118.734	-3.21E-01	-4.90E-01	1 Unchanged Low
Q15053	G14gh1	KIAA040 gene product	111.1705	146	113.5775	123.496	3.09E-02	3.91E-01	1 Unchanged Low
P22301	H01ef7	Interleukin 10	174.8595	108	113.5877	132.021	-6.22E-01	-7.00E-01	1 Unchanged Low
Q9BW47	N12gh5	chromosome 20 open reading fr	125.8269	154	113.6221	131.1841	-1.47E-01	2.92E-01	1 Unchanged Low
P21917	M03ab6	dopamine receptor D4	158.6974	151	113.7899	141.2355	-4.80E-01	-6.96E-02	1 Unchanged Low
Q9Y6K5	M19cd1	2'-5'-oligoadenylate synthetase 3	127.2648	142	113.9993	127.6931	-1.59E-01	1.56E-01	1 Unchanged Low
Q9Y2A4	N22cd5	Krppel-type zinc finger (C2H2)	136.0849	133	114.1395	127.5854	-2.54E-01	-3.82E-02	1 Unchanged Low
Q16580	A16cd3	UDP glycosyltransferase 8 (UDP	112.9309	133	114.1612	119.9407	1.56E-02	2.33E-01	1 Unchanged Low
Q95747	D09cd5	oxidative-stress responsive 1	113.39	123	114.2384	116.7318	1.08E-02	1.12E-01	1 Unchanged Low
P25106	L12ef4	G protein-coupled receptor	100.7123	147	114.2482	120.5368	1.82E-01	5.42E-01	1 Unchanged Low
	H23ab5	immunoglobulin superfamily; me	102.6971	145	114.3219	120.6924	1.55E-01	4.98E-01	1 Unchanged Low
P45984	L18ef5	mitogen-activated protein kinase	139.4168	88	114.3405	113.914	-2.86E-01	-6.64E-01	1 Unchanged Low
Q9NP77	I03ef3	Interleukin 23; alpha subunit p19	98.83593	182	114.4153	131.5891	2.11E-01	8.77E-01	1 Unchanged Low
Q9UH94	L07cd8	prolactin regulatory element bind	140.4102	106	114.4158	120.3231	-2.95E-01	-4.04E-01	1 Unchanged Low
Q16559	F05cd2	T-cell acute lymphocytic leukemia	131.4974	111	114.5482	118.9991	-1.99E-01	-2.45E-01	1 Unchanged Low
Q9UH0	C02cd8	solute carrier family 17 (anion/su	98.73308	158	114.6616	123.6748	2.16E-01	6.75E-01	1 Unchanged Low
Q15544	J13cd2	TAF11 RNA polymerase II; TATA	117.4634	123	114.6792	118.4317	-3.46E-02	6.82E-02	1 Unchanged Low
Q00628	N24ab7	peroxisomal biogenesis factor 7	156.16	96.3	114.7281	122.588	-4.45E-01	-6.69E-01	1 Unchanged Low
O43241	F07ab5	golgi autoantigen; golgin subfam	123.9421	104	114.8381	114.422	-1.10E-01	-2.46E-01	1 Unchanged Low
Q9Y6N1	M14ab4	COX11 homolog; cytochrome c c	127.1203	100	114.8993	114.0578	-1.46E-01	-3.44E-01	1 Unchanged Low
Q9UHD5	O01ef4	HT002 protein; hypertension-relat	98.26523	155	114.9242	122.8348	2.26E-01	6.60E-01	1 Unchanged Low
Q01664	A02cd2	transcription factor AP-4 (activat	268.3453	66.7	115.0377	150.0321	-1.22E+00	-2.01E+00	1 Unchanged Low
Q9BUJ1	O03gh6	leukocyte receptor cluster (LRC)	112.2417	125	115.039	117.3611	3.55E-02	1.53E-01	1 Unchanged Low
Q9HBL5	M17gh4	AD023 protein	103.9999	137	115.0443	118.5457	1.46E-01	3.93E-01	1 Unchanged Low
Q9NXK2	N08gh2	hypothetical protein FLJ20040	126.6647	147	115.1386	129.6462	-1.38E-01	2.16E-01	1 Unchanged Low
Q15424	D08cd1	scaffold attachment factor B	134.9613	92.7	115.1845	114.2781	-2.29E-01	-5.42E-01	1 Unchanged Low
P26440	F06ab6	isovaleryl Coenzyme A dehydrog	178.7093	115	115.2412	136.2534	-6.33E-01	-6.38E-01	1 Unchanged Low
O60264	J11cd3	SWI/SNF related; matrix associ	105.7775	132	115.2498	117.7402	1.24E-01	3.22E-01	1 Unchanged Low
Q15286	K07cd7	RAB35; member RAS oncogene	138.2766	183	115.3443	145.6	-2.62E-01	4.06E-01	1 Unchanged Low
Q9UH0	I10ef4	D1P8 protein	303.2745	172	115.4096	196.7868	-1.39E+00	-8.21E-01	1 Unchanged Low
Q92980	J06cd5	putative protein similar to nessy I	142.089	181	115.4166	146.2003	-3.00E-01	3.50E-01	1 Unchanged Low
Q99726	M06cd3	solute carrier family 30 (zinc tran	112.8008	121	115.4854	116.3247	3.39E-02	9.75E-02	1 Unchanged Low
P01111	O17ab8	neuroblastoma RAS viral (v-ras)	123.6263	108	115.5932	115.8629	-9.70E-02	-1.90E-01	1 Unchanged Low
Q92574	G13cd3	tuberous sclerosis 1	109.8519	128	115.7107	117.8303	7.50E-02	2.20E-01	1 Unchanged Low

P16106	C01gh7	H3 histone family; member 1	134.9364	118	115.868	122.8016	-2.20E-01	-1.98E-01	1	Unchanged Low
Q9NWX5	O24gh2	hypothetical protein FLJ20548	118.1581	112	115.9919	115.5043	-2.67E-02	-7.26E-02	1	Unchanged Low
Q9Y6B7	M05ab3	adaptor-related protein complex	217.8572	170	116.0173	168.0108	-9.09E-01	-3.57E-01	1	Unchanged Low
Q9Y4F1	J04cd5	FERM; RhoGEF (ARHGEF) and	108.6215	130	116.0342	118.0819	9.52E-02	2.56E-01	1	Unchanged Low
Q06710	M14cd3	paired box gene 8	120.1357	129	116.1006	121.7641	-4.93E-02	1.03E-01	1	Unchanged Low
Q9HGN1	J17gh5	hypothetical protein FLJ22056	214.4909	242	116.2509	190.8582	-8.84E-01	1.73E-01	1	Unchanged Low
Q9NSV1	K09gh3	homolog of mouse BMP-2 Inducd	111.9034	123	116.2514	117.0914	5.50E-02	1.38E-01	1	Unchanged Low
Q14106	H20cd6	transducer of ERBB2; 2	117.9634	134	116.2536	122.8358	-2.11E-02	1.87E-01	1	Unchanged Low
Q9UK11	B02ef4	zinc finger protein 223	119.1221	133	116.2873	122.6322	-3.47E-02	1.60E-01	1	Unchanged Low
P08069	O17ef6	insulin-like growth factor 1 recept	106.3434	178	116.3103	133.4883	1.29E-01	7.42E-01	1	Unchanged Low
Q9HF5	I21gh6	hypothetical protein MGC2574	120.5097	112	116.3129	116.1638	-5.11E-02	-1.10E-01	1	Unchanged Low
Q14373	O04ab3	galactose-1-phosphate uridylyl	157.7476	231	116.3555	168.3955	-4.39E-01	5.51E-01	1	Unchanged Low
P20393	G04ef5	nuclear receptor subfamily 1; gro	107.1138	138	116.4228	120.571	1.20E-01	3.67E-01	1	Unchanged Low
P36915	O01ab5	guanine nucleotide binding prote	120.9306	111	116.4819	116.2706	-5.41E-02	-1.18E-01	1	Unchanged Low
Q95109	G02cd8	chromosome 20 open reading fr	143.5728	103	116.5321	121.0452	-3.01E-01	-4.79E-01	1	Unchanged Low
Q9NV52	I24gh3	mitochondrial ribosomal protein t	117.9573	124	116.6011	119.5497	-1.67E-02	7.31E-02	1	Unchanged Low
Q92850	B08cd6	CUO triplet repeat; RNA binding	109.8876	129	116.7366	118.6125	8.72E-02	2.34E-01	1	Unchanged Low
Q14977	C04ab7	SP110 nuclear body protein	107.0969	158	116.8973	127.3783	1.26E-01	5.62E-01	1	Unchanged Low
P16106	O04gh6	H3 histone family; member A	94.76745	159	116.9796	123.5385	3.04E-01	7.45E-01	1	Unchanged Low
Q9Y3C1	N18ef2	hypothetical protein HSPC111	145.1935	164	117.0185	141.934	-3.11E-01	1.72E-01	1	Unchanged Low
P37287	C11ef1	phosphatidylinositol glycan; clas	132.5354	109	117.2467	119.4716	-1.77E-01	-2.87E-01	1	Unchanged Low
Q9UIG5	G05ef4	SEEK1 protein	102.5149	148	117.279	122.443	1.94E-01	5.25E-01	1	Unchanged Low
Q9UNE2	G15cd6	rabphilin 3A-like (without C2 do	110.3023	123	117.2874	117.0111	8.86E-02	1.62E-01	1	Unchanged Low
Q14123	A17cd1	phosphodiesterase 1C; calmodul	121.3078	132	117.3754	123.5304	-4.75E-02	1.21E-01	1	Unchanged Low
Q16208	P03ab2	cystolic ovarian carcinoma ant	116.5183	157	117.4492	130.1671	1.15E-02	4.26E-01	1	Unchanged Low
Q9NWV1	D21gh2	hypothetical protein FLJ20624	116.0517	116	117.4816	116.4708	1.77E-02	-2.15E-03	1	Unchanged Low
Q12756	C05ab3	axonal transport of synaptic vest	138.4398	232	117.5489	162.7767	-2.36E-01	7.47E-01	1	Unchanged Low
P28288	B10ab6	ATP-binding cassette; sub-family	140.4464	95.9	117.5959	117.9574	-2.56E-01	-5.51E-01	1	Unchanged Low
P05198	G08ab5	eukaryotic translation initiation fa	115.5074	119	117.6033	117.2266	2.59E-02	3.77E-02	1	Unchanged Low
Q9H0V9	D08gh7	hypothetical protein DKFZp564L	128.832	101	117.6689	115.9248	-1.31E-01	-3.47E-01	1	Unchanged Low
Q92984	M10ef1	interferon-induced protein 35	258.0737	221	117.8182	198.9799	-1.13E+00	-2.23E-01	1	Unchanged Low
Q95498	A13cd5	vanin 2	109.7731	123	117.8273	116.8572	1.02E-01	1.64E-01	1	Unchanged Low
Q9H1E1	J01gh8	ribonuclease 7	109.332	131	117.8377	119.4295	1.08E-01	2.62E-01	1	Unchanged Low
Q9NV88	H01gh3	hypothetical protein FLJ10871	108.5849	125	117.8411	117.172	1.18E-01	2.04E-01	1	Unchanged Low
Q9Y310	F06cd6	SnRNP assembly defective 1 hor	119.9305	113	117.8563	117.0556	-2.52E-02	-8.10E-02	1	Unchanged Low
P48382	O06cd1	regulatory factor X; 5 (Influences	191.5142	122	118.0773	143.9771	-6.98E-01	-6.47E-01	1	Unchanged Low
P52738	K04cd3	zinc finger protein 140 (done pH)	136.6566	154	118.1501	136.2205	-2.10E-01	1.71E-01	1	Unchanged Low
Q9NRW1	G23er3	RAB8B; member RAS oncogene	100.578	179	118.1659	132.4668	2.32E-01	8.29E-01	1	Unchanged Low
Q15298	A02ab3	basic leucine zipper nuclear fact	266.9887	110	118.2062	165.1797	-1.18E+00	-1.27E+00	1	Unchanged Low
Q9UN5	D14gh3	hypothetical protein FLJ1240	114.5392	116	118.2691	116.1573	4.62E-02	1.41E-02	1	Unchanged Low
Q07699	L03cd1	sodium channel; voltage-gated; I	116.5431	113	118.3239	115.8757	2.19E-02	-4.76E-02	1	Unchanged Low
P27701	F10ab6	kangal 1 (suppression of tumorig	116.2761	108	118.3861	114.2624	2.60E-02	-1.05E-01	1	Unchanged Low
Q9UER5	O02er3	TNF-induced protein	104.9755	131	118.4653	118.2694	1.74E-01	3.24E-01	1	Unchanged Low
Q8TAC6	I24gh7	chromosome 11 open reading fr	117.4257	138	118.5867	124.5093	1.42E-02	2.28E-01	1	Unchanged Low
Q9NRW9	K16gh4	angiotensin II; type I receptor-α	136.6357	105	118.6777	120.1907	-2.03E-01	-3.76E-01	1	Unchanged Low
Q95147	O15cd7	dual specificity phosphatase 14	181.9968	200	118.7007	166.9415	-6.17E-01	1.37E-01	1	Unchanged Low
Q13695	A19ef7	bystin-like	108.0232	124	118.7967	116.9004	1.37E-01	1.98E-01	1	Unchanged Low
P31645	N03ef5	solute carrier family 6 (neurotran	114.6464	189	118.8487	140.7231	5.19E-02	7.19E-01	1	Unchanged Low
P51111	N17ef7	matrix metalloproteinase 15 (mer	122.9018	125	118.8609	122.1739	-4.82E-02	2.16E-02	1	Unchanged Low
Q15154	O11cd1	pericentriolar material 1	127.8378	139	118.8759	128.7076	-1.05E-01	1.25E-01	1	Unchanged Low
Q90007	E7ef6	protein phosphatase 2 (formerly:	108.364	123	118.9838	116.7703	1.35E-01	1.82E-01	1	Unchanged Low
P55822	L08cd2	SH3 domain containing glutamic acid	131.7189	133	119.0263	128.0275	-1.46E-01	1.76E-02	1	Unchanged Low
Q14442	D20ab9	phosphatidylinositol glycan; clas	121.0635	114	119.0306	118.0476	-2.44E-02	-8.61E-02	1	Unchanged Low
P54792	L04ab4	dishevelled; dsh homolog 1 (Dro	126.677	113	119.067	119.4338	-8.94E-02	-1.70E-01	1	Unchanged Low
P42336	A03ef6	phosphoinositide-3-kinase; catal	101.0905	143	119.1581	121.01	2.37E-01	4.98E-01	1	Unchanged Low
Q9UMQ3	G15ab3	Bar-Hillel homeobox 2	99.5713	179	119.1741	132.6879	2.59E-01	8.49E-01	1	Unchanged Low
Q9UPY5	M04ef3	solute carrier family 7; (cationic ε	133.9407	69.5	119.3079	120.9226	-5.44E-01	-1.32E+00	1	Unchanged Low
P19113	H01ef6	histidine decarboxylase	111.9277	119	119.3155	116.6743	9.22E-02	8.57E-02	1	Unchanged Low
Q95394	B16ef3	N-acetylglucosamine-phosphate	124.8164	112	119.3184	118.8198	-6.50E-02	-1.52E-01	1	Unchanged Low
P22557	A14ab2	aminolevulinic; delta-; synthase	202.1179	129	119.3857	150.2281	-7.60E-01	-6.46E-01	1	Unchanged Low
Q9Y3A2	G10ef2	CGI-94 protein	108.7497	167	119.4751	131.6512	1.36E-01	6.16E-01	1	Unchanged Low
Q9H5J4	I05gh6	long-chain fatty-acyl elongase	135.0119	87	119.5181	113.8461	-1.76E-01	-6.34E-01	1	Unchanged Low
P16083	E15ab8	NAD(P)H dehydrogenase; quinol	154.7986	98.6	119.5724	124.3296	-3.73E-01	-6.50E-01	1	Unchanged Low
Q99819	D02ab2	Rho GDP dissociation inhibitor (C	125.7962	106	119.5853	117.2457	-7.30E-02	-2.42E-01	1	Unchanged Low
Q75569	F06cd3	protein kinase; Interferon-Induced	100.3086	137	119.6257	118.9057	2.54E-01	4.47E-01	1	Unchanged Low
O15038	F12ef7	serine/arginine repetitive matrix 2	125.19	95.6	119.719	113.8294	-6.45E-02	-3.74E-01	1	Unchanged Low
Q9HBH5	K09gh4	PAN2 protein	102.0601	139	119.7321	120.3437	2.30E-01	4.48E-01	1	Unchanged Low
P41231	C22ab8	purinergic receptor P2Y; G-prote	131.9219	130	119.8105	127.3275	-1.39E-01	-1.84E-02	1	Unchanged Low
O15397	D01cd6	RAN binding protein 8	114.6925	118	119.9197	117.4304	6.43E-02	3.71E-02	1	Unchanged Low
Q9UDY8	C17cd7	mucosa associated lymphoid tiss	114.4769	120	119.9403	118.129	6.73E-02	6.76E-02	1	Unchanged Low
Q95819	E22cd5	mitogen-activated protein kinase	92.42403	156	119.956	122.7769	3.76E-01	7.55E-01	1	Unchanged Low
Q12999	J01ef5	sarcoma amplified sequence	114.9397	110	119.9579	114.8641	6.17E-02	6.74E-02	1	Unchanged Low
P25440	D07od2	bromodomain containing 2	116.6707	108	120.0152	114.7701	4.08E-02	-1.16E-01	1	Unchanged Low
P20827	H21ef7	ephrin-A1	298.0458	760	120.3333	392.8203	-1.31E+00	1.35E+00	1	Unchanged Low
Q9H652	P20gh8	hypothetical protein MGC4171	129.5733	107	120.4428	118.9065	-1.05E-01	-2.80E-01	1	Unchanged Low
P31483	L20ef4	TIA1 cytosolic granule-associlate	105.4425	129	120.5366	118.2227	1.93E-01	2.87E-01	1	Unchanged Low
Q9BSM8	G15gh8	hypothetical protein MGC10812	148.2279	273	120.5724	180.6391	-2.98E-01	8.82E-01	1	Unchanged Low
P36897	F04ef5	transforming growth factor; beta 1	115.7567	108	120.6724	114.8546	6.00E-02	-9.83E-02	1	Unchanged Low
Q9UMR9	E08ef3	YME1-like 1 (S. cerevisiae)	256.0314	197	120.7227	191.0958	-1.08E+00	-3.82E-01	1	Unchanged Low
Q92560	G11ab3	BRCA1 associated protein-1 (ubl	101.36	161	120.7575	127.8687	2.53E-01	6.72E-01	1	Unchanged Low
Q9NWU1	D05gh2	hypothetical protein FLJ20604	99.76081	154	120.7609	124.8325	2.76E-01	6.26E-01	1	Unchanged Low
Q92636	N14ab8	Rab geranylgeranyltransferase; t	222.7157	272	120.7706	205.3234	-8.83E-01	2.91E-01	1	Unchanged Low
Q95236	M24ef3	apoflipoprotein L; 3	106.592	130	120.798	119.1528	1.80E-01	2.87E-01	1	Unchanged Low
Q13202	E21ab5	dual specificity phosphatase 8	146.3963	129	120.7987	131.9045	-2.77E-01	-1.68E-01	1	Unchanged Low
P11277	M02cd1	spectrin; beta; erythrocytic (indu	112.72	114	120.8055	116.0084	9.99E-02	2.26E-02	1	Unchanged Low
Q95397	P18ef1	putative glycolipid transfer prote	99.78536	143	120.8708	121.1071	2.77E-01	5.16E-01	1	Unchanged Low

P05423	A20ab3	BN51 (BHK21) temperature sens	131.8122	95.5	120.9201	116.0734	-1.24E-01	-4.65E-01	1	Unchanged Low
Q14338	I17ab6	fucosyltransferase 2 (secretor srt	99.71915	181	120.9483	133.9938	2.78E-01	8.63E-01	1	Unchanged Low
Q9BY18	A22gh8	AI6-75 binding protein protein	90.11911	164	121.0209	125.1664	4.25E-01	8.67E-01	1	Unchanged Low
Q06203	D01ab8	phosphoribosyl pyrophosphate a	216.3154	105	121.029	147.3953	-8.38E-01	-1.04E+00	1	Unchanged Low
Q9NZ33	P10gh4	brain expressed; X-linked 1	113.8613	162	121.0508	132.4428	8.83E-02	5.12E-01	1	Unchanged Low
P04196	O10ab6	histidine-rich glycoprotein	116.1305	116	121.1163	117.5882	6.06E-02	-7.63E-03	1	Unchanged Low
Q96029	F03cd7	opiod growth factor receptor	201.3579	93.5	121.2888	138.7174	-7.31E-01	-1.11E+00	1	Unchanged Low
Q01196	I16ab5	runt-related transcription factor 1	441.1217	136	121.3316	232.9078	-1.86E+00	-1.69E+00	1	Unchanged Low
Q9UHL4	J17cd8	dipeptidylpeptidase 7	180.3445	191	121.351	164.207	-5.72E-01	8.23E-02	1	Unchanged Low
P55211	P16ab3	caspase 9; apoptosis-related cys	113.5416	111	121.3742	115.3899	9.62E-02	-2.94E-02	1	Unchanged Low
P21283	A07ab3	ATPase; H <sup>+</sup> transporlting; lysoso	288.6034	288	121.3828	232.7446	-1.25E+00	-1.78E-03	1	Unchanged Low
O43422	P02ab8	protein-kinase; interferon-induct	131.8635	100	121.394	117.7416	-1.19E-01	-4.00E-01	1	Unchanged Low
P78406	L01cd3	RAE1 RNA export 1 homolog (S.	147.1192	97.1	121.4625	121.9098	-2.76E-01	-5.99E-01	1	Unchanged Low
P43362	J18ab7	melanoma antigen; family A; 9	99.05783	139	121.5326	119.97	2.95E-01	4.92E-01	1	Unchanged Low
Q9H693	E12gh6	hypothetical protein FLJ22477	171.7699	96.4	121.6097	129.9396	-4.98E-01	-8.33E-01	1	Unchanged Low
Q9UJB3	A11cd8	2-hydroxyphthalanoyl-CoA lyase	99.45467	141	121.6399	120.5495	2.91E-01	4.99E-01	1	Unchanged Low
Q05048	I15ab4	cleavage stimulatory factor; 3'	124.1609	105	121.6764	117.088	-2.92E-02	-2.36E-01	1	Unchanged Low
P19784	D11ab4	casein kinase 2; alpha prime pol	94.68573	152	121.7819	122.6579	3.63E-01	6.78E-01	1	Unchanged Low
Q9BUX8	D06gh6	homolog of yeast ribosome bioge	167.4752	178	121.8214	155.6701	-4.59E-01	5.65E-02	1	Unchanged Low
Q9Y5P6	D23cd8	GDP-mannose pyrophosphoryl	166.4572	89.4	121.8219	125.8828	-4.50E-01	-8.97E-01	1	Unchanged Low
Q9Y3E1	F16ef1	hepatoma-derived growth factor;	97.00713	148	121.9163	122.172	3.30E-01	6.05E-01	1	Unchanged Low
P40426	O07cd1	pre-B-cell leukemia transcription	122.6888	94.8	121.9253	113.1427	-9.01E-03	-3.72E-01	1	Unchanged Low
P11217	K01cd1	phosphorylase; glycogen; muscle	314.8041	110	122.0008	182.286	-1.37E+00	-1.52E+00	1	Unchanged Low
Q16563	D18cd2	synaptophysin-like protein	97.62823	144	122.0944	121.3173	3.23E-01	5.63E-01	1	Unchanged Low
Q95698	L07ab6	Inhibitor of growth family; membe	102.2388	135	122.1358	119.6732	2.57E-01	3.97E-01	1	Unchanged Low
P19447	K24ef6	excision repair cross-complemen	95.41189	148	122.1425	121.7265	3.56E-01	6.30E-01	1	Unchanged Low
Q9UIC39	D08cd7	CCR4 carbon catabolite repress	173.8761	262	122.1589	185.8825	-5.09E-01	5.89E-01	1	Unchanged Low
Q15785	E23cd7	translocase of outer mitochondrial	296.8521	144	122.1776	187.6861	-1.28E+00	-1.04E+00	1	Unchanged Low
Q99571	C14ab8	purinergic receptor P2X; ligand-	418.1812	410	122.3053	316.7241	-1.77E-00	-2.95E-02	1	Unchanged Low
Q9BTY2	E24gh8	hypothetical protein MGC1314 si	131.9449	91.5	122.3524	115.258	-1.09E-01	-5.28E-01	1	Unchanged Low
Q9P0P1	D12ef1	hypothetical protein FLJ10769	147.9172	191	122.4861	153.8845	-2.72E-01	3.71E-01	1	Unchanged Low
Q9Y324	P01ef1	CGI-35 protein	129.1118	97	122.5531	116.2093	-7.52E-02	-4.13E-01	1	Unchanged Low
P37286	O17cd3	ubiquitin-conjugating enzyme E2	98.88763	165	122.5569	128.7921	3.10E-01	7.38E-01	1	Unchanged Low
Q00577	O07ef5	purine-rich element binding prote	116.0341	123	122.5705	120.658	7.91E-02	8.84E-02	1	Unchanged Low
O75152	L21gh1	KIAA0663 gene product	101.4464	140	122.5789	121.2139	2.73E-01	4.61E-01	1	Unchanged Low
P23610	H06cd7	coagulation factor VII-associated	164.911	103	122.5902	130.3149	-4.28E-01	-6.73E-01	1	Unchanged Low
O75436	M20cd5	vacuolar protein sorting 26 (ves	118.1135	108	122.6522	116.2363	5.44E-02	-1.30E-01	1	Unchanged Low
Q9HA40	B23gh5	hypothetical protein FLJ12287 si	104.6286	126	122.666	117.8494	2.29E-01	2.71E-01	1	Unchanged Low
Q9NX62	I20gh2	hypothetical protein FLJ20421	103.7764	136	122.701	120.752	2.42E-01	3.88E-01	1	Unchanged Low
O76062	E04cd2	transmembrane 7 superfamily me	301.1903	215	122.7645	212.8749	-1.29E+00	-4.89E-01	1	Unchanged Low
Q16445	H02ab3	gamma-aminobutyric acid (GABA)	150.641	87.5	122.7829	120.3177	-2.95E-01	-5.63E-01	1	Unchanged Low
Q08462	G11ef6	adenylyl cyclase 2 (brain)	107.541	146	122.8502	125.3933	1.92E-01	4.39E-01	1	Unchanged Low
P78560	A22ef6	CASP2 and RIPK1 domain conta	108.4508	153	122.8627	128.1152	1.80E-01	4.97E-01	1	Unchanged Low
P19634	N17ef5	solute carrier family 9 (sodium/h)	118.9969	99	122.8828	113.6214	4.65E-02	-2.66E-01	1	Unchanged Low
P28370	N12cd1	SW/SNf related; matrix associa	115.471	106	122.9184	114.9572	9.02E-02	-1.17E-01	1	Unchanged Low
Q92503	H06cd1	SEC14-like 1 (S. cerevlsae)	151.5939	151	122.9424	141.9225	-3.02E-01	-3.46E-03	1	Unchanged Low
Q9UL02	H24ef1	L-kyurenine/alpha-aminoadipate	105.6951	124	123.0487	117.4294	2.19E-01	2.25E-01	1	Unchanged Low
Q9Y5T5	J13cd6	ubiquitin specific protease 16	117.1056	120	123.0646	120.0007	7.16E-02	3.32E-02	1	Unchanged Low
P15848	H02ab2	proteocadherin 15	153.0978	126	123.1548	134.1729	-3.14E-01	-2.78E-01	1	Unchanged Low
Q9UP66	P24ab6	arylsulfatase B	149.4791	95.6	123.1651	122.7499	-2.79E-01	-6.45E-01	1	Unchanged Low
Q75160	P07gh1	low density lipoprotein receptor-r	114.2435	124	123.2083	120.4437	1.09E-01	1.17E-01	1	Unchanged Low
P78385	L14ab6	KIAA0672 gene product	121.9398	117	123.2554	120.8501	1.55E-02	-5.53E-02	1	Unchanged Low
O94967	B21ef8	keratin; hair; basic; 3	100.703	135	123.2569	119.6793	2.92E-01	4.24E-01	1	Unchanged Low
Q95719	K01cd5	xenotropic and polytropic retrov	108.0877	158	123.2707	124.6247	4.20E-01	7.82E-01	1	Unchanged Low
P48147	F09ab8	prolyl endopeptidase	130.0641	122	123.3497	117.7043	1.91E-01	1.71E-01	1	Unchanged Low
P20231	B15gh7	tryptase beta 2	106.6865	130	123.4905	119.9323	2.11E-01	2.81E-01	1	Unchanged Low
Q95299	G02ab7	NADH dehydrogenase (ubiquinol)	107.385	129	123.5591	119.8634	2.03E-01	2.60E-01	1	Unchanged Low
O75033	I18gh1	KIAA0445 gene product	121.5196	122	123.624	122.4835	2.48E-02	9.32E-03	1	Unchanged Low
P51668	D03cd4	ubiquitin-conjugating enzyme E2	99.84401	137	123.6337	120.3	3.08E-01	4.61E-01	1	Unchanged Low
P28289	E08cd2	tropomodulin	303.877	272	123.6484	233.0271	-1.30E-00	-1.52E-01	1	Unchanged Low
Q15631	O12ef6	translin	173.134	152	123.6887	149.5989	-4.85E-01	-1.88E-01	1	Unchanged Low
P49888	F03cd2	sulfotransferase; estrogen-prefer	122.2586	95.1	123.7564	113.6937	1.76E-02	-3.63E-01	1	Unchanged Low
P51959	O12ef5	cyclin G1	116.6841	102	123.7651	114.0387	8.50E-02	-1.99E-01	1	Unchanged Low
Q9Y5V0	J16ef1	HSPC038 protein	114.0123	179	123.7922	139.0584	1.19E-01	6.54E-01	1	Unchanged Low
P56270	I12ef1	MYC-associated zinc finger pro	248.3395	140	123.8618	170.7774	-1.00E-00	-8.26E-01	1	Unchanged Low
Q9HD23	O11gh4	MRS2-like; magnesium homeost	140.8864	117	123.8621	127.1502	-1.86E-01	-2.72E-01	1	Unchanged Low
P78358	O03ab6	cancer/testis antigen 1	217.9167	137	123.9307	159.681	-8.14E-01	-6.68E-01	1	Unchanged Low
O00327	D24ab2	aryl hydrocarbon receptor nucle	118.2008	165	123.9691	142.5298	6.87E-02	6.50E-01	1	Unchanged Low
Q9H969	F08gh5	hypothetical protein FLJ12689	89.23821	177	124.0248	130.1172	4.75E-01	9.89E-01	1	Unchanged Low
O15504	F01cd7	nudeoeporin-like protein 1	200.4449	124	124.2046	149.5876	-6.90E-01	-6.92E-01	1	Unchanged Low
P35250	I24ef6	replication factor C (activator 1)	111.3418	112	124.3534	115.9922	1.59E-01	1.21E-02	1	Unchanged Low
Q9BX0	F17gh8	G protein-coupled receptor 81	104.4833	128	124.3568	118.786	2.51E-01	2.87E-01	1	Unchanged Low
O15232	A19ef1	mannin 3	113.1634	110	124.4317	115.8185	1.37E-01	-4.27E-02	1	Unchanged Low
Q76049	L19cd5	specrin SH3 domain binding pro	171.9625	299	124.5037	198.6303	-4.66E-01	8.00E-01	1	Unchanged Low
Q14145	C21cd8	Kelch-like ECH-associated prote	193.9671	120	124.5928	146.2645	-6.39E-01	-6.90E-01	1	Unchanged Low
P20848	A10cd1	serine (or cysteine) proteinase	97.77909	161	124.6004	127.9292	3.50E-01	7.23E-01	1	Unchanged Low
Q9P0N6	C19ef3	hypothetical protein HSPC242	112.0065	109	124.6034	115.304	1.54E-01	-3.53E-02	1	Unchanged Low
P05188	E12ab2	alkaline phosphatase; placental	88.50098	164	124.6125	125.869	4.94E-01	8.94E-01	1	Unchanged Low
Q9UBJ4	A01gh5	transposon-derived Buster1 tran	131.0923	97.3	124.7023	117.695	-7.21E-02	-4.30E-01	1	Unchanged Low
Q13876	I24ef7	quiescin Q6	144.3305	109	124.7205	125.9829	-2.11E-01	-4.06E-01	1	Unchanged Low
Q9UBF2	F12cd7	coatomer protein complex; subu	110.1673	115	124.9117	116.849	1.81E-01	6.78E-02	1	Unchanged Low
P43026	I23cd3	growth differentiation factor 5 (ca	101.9864	152	124.9218	126.3658	2.93E-01	5.77E-01	1	Unchanged Low
Q9HD20	E14gh4	CGI-152 protein	111.6731	134	124.9301	123.6472	1.62E-01	2.67E-01	1	Unchanged Low
Q96KK6	P04ab8	RAB2; member RAS oncogene ft	119.8171	106	124.9467	116.8445	6.05E-02	-1.80E-01	1	Unchanged Low
P40617	D18ab2	ADP-ribosylation factor-like 4	124.1402	143	125.0573	130.7449	1.06E-02	2.04E-01	1	Unchanged Low

O75651	L12gh2	unc-93 homolog A (C. elegans)	131.989	128	125.0667	128.2583	-7.77E-02	-4.74E-02	1 Unchanged Low
Q9Y251	L04ef1	galanin-related peptide	135.6724	134	125.067	131.4639	-1.17E-01	-2.10E-02	1 Unchanged Low
Q13330	M20ef5	melastasis associated 1	104.9962	118	125.1131	116.0949	2.53E-01	1.71E-01	1 Unchanged Low
Q9Y389	L22gh4	amino adipate-semialdehyde dehydrolase	115.3352	104	125.222	114.7055	1.19E-01	-1.55E-01	1 Unchanged Low
O60513	I03gh1	UDP-Gal-betaGlcNAc beta 1:4- $\alpha$	113.705	106	125.2504	115.0129	1.40E-01	-1.00E-01	1 Unchanged Low
O00212	C15ef6	ras homolog gene family; member 4	107.7018	492	125.2682	341.5179	-1.70E+00	2.70E-01	1 Unchanged Low
Q9NXE1	J04gh2	membrane-associated nucleic acid	96.25484	146	125.3861	122.4125	3.81E-01	5.97E-01	1 Unchanged Low
O95405	A16cd5	MAD; mothers against decapentapetide	113.9303	223	125.3908	154.2554	1.38E-01	9.72E-01	1 Unchanged Low
P01112	K12ab7	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	129.7326	104	125.3947	119.6125	-4.91E-02	-3.23E-01	1 Unchanged Low
O15120	F11cd6	1-acylglycerol-3-phosphate O-acyl transferase	264.2959	238	125.4039	209.3705	-1.08E+00	-1.49E-01	1 Unchanged Low
P12645	N10ab3	bone morphogenetic protein 3 (ο)	107.6548	117	125.4244	116.6372	2.20E+00	1.18E-01	1 Unchanged Low
P50579	I01cd7	methionyl aminopeptidase 2	144.5653	95.1	125.4613	121.7158	-2.05E-01	-6.04E-01	1 Unchanged Low
O14908	K01cd6	regulator of G-protein signalling	204.527	200	125.5241	176.6683	-7.04E-01	-3.26E-02	1 Unchanged Low
Q9HCC6	I17gh4	bHLH factor Hes4	82.07655	213	125.5621	140.2118	6.13E-01	1.38E+00	1 Unchanged Low
Q15737	E23gh1	suppressor of Ty 6 homolog (S. pombe)	112.2771	140	125.5917	125.8246	1.62E-01	3.14E-01	1 Unchanged Low
Q9Y519	A17cd8	chromosome 22 open reading frame	100.4037	131	125.6586	119.1056	3.24E-01	3.87E-01	1 Unchanged Low
Q9Y5J0	J01ef2	mitochondrial ribosomal protein L	117.4353	107	125.8555	116.7986	9.99E-02	-1.33E-01	1 Unchanged Low
P51667	O16cd1	sulfite oxidase	105.2314	128	125.9497	119.5637	2.59E-01	2.77E-01	1 Unchanged Low
P51178	A13ef6	phospholipase C; delta 1	126.4221	162	126.0345	138.0904	-4.43E-03	3.56E-01	1 Unchanged Low
Q9H8J6	H23gh5	NDRG family member 3	121.7115	198	126.0448	148.4766	5.05E-02	7.00E-01	1 Unchanged Low
O95900	B20ef8	hypothetical protein CLONE2492	165.6404	257	126.0637	182.7338	-3.94E-01	6.31E-01	1 Unchanged Low
Q9Y6N3	B01cd5	chloride channel; calcium activator	99.89597	135	126.1695	120.3564	3.37E-01	4.35E-01	1 Unchanged Low
Q70869	C21cd1	peroxisome proliferative activated receptor	120.1031	112	126.2127	119.4872	7.16E-02	-9.89E-02	1 Unchanged Low
Q9Y333	I07gh4	chromosome 6 open reading frame	109.0761	114	126.2563	116.4501	2.11E-01	6.39E-02	1 Unchanged Low
Q9NPD1	L06gh2	G protein-coupled receptor 85	206.0578	285	126.2683	205.7432	-7.07E-01	4.67E-01	1 Unchanged Low
Q15928	K06cd3	zinc finger protein 141 (clone pH)	101.1559	188	126.2732	138.6304	3.20E-01	6.98E-01	1 Unchanged Low
O43826	I04ab4	glucose-6-phosphatase; transpoter	229.7084	111	126.3113	155.5451	-8.63E-01	-1.05E+00	1 Unchanged Low
Q9NW0L	J05gh2	hypothetical protein FLJ20758	114.0453	120	126.3891	120.1186	1.48E-01	7.25E-02	1 Unchanged Low
P31629	B04ef6	human immunodeficiency virus type 1	116.0174	211	126.4284	151.1911	1.24E-01	6.64E-01	1 Unchanged Low
O15530	I10ab8	3-phosphoinositide dependent protein kinase	186.1234	193	126.45	168.488	-5.58E-01	5.15E-02	1 Unchanged Low
Q9Y2R5	L21ef4	mitochondrial ribosomal protein S	106.3741	136	126.4713	122.8701	2.50E-01	3.52E-01	1 Unchanged Low
Q15208	D01cd7	serine/threonine kinase 38	158.8765	204	126.5253	163.2891	-3.28E-01	3.64E-01	1 Unchanged Low
Q9UET6	J19gh6	FtsJ homolog (E. coli)	102.5266	120	126.5378	116.4386	3.04E-01	2.30E-01	1 Unchanged Low
Q9HSN0	F15gh5	chromosome 7 open reading frame	102.3349	129	126.5687	119.1911	3.07E-01	3.30E-01	1 Unchanged Low
Q9H019	B22gh4	hypothetical protein RP1-317E23	102.5329	150	126.5974	126.5367	3.04E-01	5.53E-01	1 Unchanged Low
Q9Y673	B05cd8	Al5g; S. cerevisiae; homolog of	100.2543	131	126.6884	119.1797	3.38E-01	3.81E-01	1 Unchanged Low
Q75690	M08gh7	UHS KerB	121.3598	150	126.7819	132.5659	6.31E-02	3.01E-01	1 Unchanged Low
Q9NUP6	H22gh2	hypothetical protein FLJ11220	95.908	144	126.8164	122.1684	4.03E-01	5.84E-01	1 Unchanged Low
Q14296	C03cd7	FAST kinase	122.4924	92.9	126.9021	114.1093	5.10E-02	-3.98E-01	1 Unchanged Low
Q9NW55	B20gh2	hypothetical protein FLJ10307	94.73914	141	126.9877	120.8058	4.23E-01	5.70E-01	1 Unchanged Low
O43638	H01cd3	NCK adaptor protein 2	139.9609	79.6	127.0299	115.5457	-1.40E-01	-8.13E-01	1 Unchanged Low
P17544	L08ab2	activating transcription factor 7	108.5839	112	127.0848	115.9726	2.27E-01	4.79E-02	1 Unchanged Low
O75911	M01cd5	short-chain dehydrogenase/reductase	156.3658	173	127.1125	152.0313	-2.99E-01	1.43E-01	1 Unchanged Low
O06430	K15ef3	glucosaminyl (N-acetyl) transferase	94.56995	139	127.1541	120.3135	4.27E-01	5.58E-01	1 Unchanged Low
Q13769	D10cd3	chromosome 22 open reading frame	122.7812	121	127.1547	123.5081	5.05E-02	-2.60E-02	1 Unchanged Low
Q9H864	J14gh5	hypothetical protein FLJ11021 sl	97.58044	142	127.1909	122.387	3.82E-01	5.45E-01	1 Unchanged Low
O95500	F06cd7	claudin 14	183.0294	181	127.2815	163.6479	-5.24E-01	-1.90E-02	1 Unchanged Low
P14222	P02cd2	perforin 1 (pore forming protein)	99.11893	135	127.3674	120.5243	3.62E-01	4.47E-01	1 Unchanged Low
Q9Y4C8	B05ef2	KIAA0682 gene product	105.4769	146	127.3803	126.2298	2.72E-01	4.67E-01	1 Unchanged Low
Q9H3H5	M23ab4	dolichyl-phosphate (UDP-N-acetyl)	193.8179	108	127.5134	143.2265	-6.04E-01	-8.39E-01	1 Unchanged Low
Q13433	G05cd8	LV-1 protein; estrogen-regulated	118.096	105	127.6623	116.7563	1.12E-01	-1.76E-01	1 Unchanged Low
Q00059	O07cd2	transcription factor A; mitochondrial	111.4615	131	127.6629	123.3486	1.96E-01	2.32E-01	1 Unchanged Low
Q15119	I06ab8	pyruvate dehydrogenase kinase	97.01115	135	127.6675	120.0132	3.96E-01	4.81E-01	1 Unchanged Low
O43791	F03cd3	speckle-type PQZ protein	111.349	114	127.7061	117.7111	1.98E-01	3.49E-02	1 Unchanged Low
Q14206	P10cd5	Down syndrome critical region gene	119.8147	263	127.7164	170.2393	9.21E-02	1.14E+00	1 Unchanged Low
Q92926	N24cd1	SWI/SNF related; matrix associator	115.147	105	127.7503	116.1179	1.50E-01	-1.27E-01	1 Unchanged Low
Q9P288	G15ef3	BRCA2 and CDKN1A interacting	148.9477	132	127.8623	136.3262	-2.20E-01	-1.72E-01	1 Unchanged Low
Q9NZU5	C16ef4	LIM and cysteine-rich domains 1	164.1438	128	127.9349	139.5949	-3.60E-01	3.61E-01	1 Unchanged Low
Q13569	O13cd2	lhydmine-DNA glycosylase	83.16502	172	127.9545	127.6936	6.22E-01	1.05E+00	1 Unchanged Low
P48167	D17ef6	glycine receptor; beta	109.5501	139	127.9738	125.3664	2.24E-01	3.39E-01	1 Unchanged Low
Q9NQR1	I02gh4	PTD/SET domain containing protein	154.2185	92.7	128.0258	124.9651	-2.69E-01	-7.35E-01	1 Unchanged Low
O43405	B23ab4	coagulation factor C homolog; cc	103.0764	121	128.1793	117.417	3.14E-01	2.31E-01	1 Unchanged Low
Q9P028	N24ef2	CCR4-NOT transcription complex	104.0341	133	128.2089	121.9053	3.01E-01	3.59E-01	1 Unchanged Low
Q9Y6E8	P04cd7	srinu silent mating type Informal	109.1684	110	128.2444	115.6628	3.23E-01	5.37E-03	1 Unchanged Low
Q9NV65	H17gh3	hypothetical protein FLJ10901	92.33747	188	128.3243	136.3568	4.75E-01	1.03E+00	1 Unchanged Low
Q9H0R8	M13gh7	GABA(A) receptor-associated protein	122.091	179	128.3386	143.1503	7.20E-02	5.52E-01	1 Unchanged Low
Q95817	P02cd4	BCL2-associated athanogene 3	107.1752	114	128.4319	116.5745	2.61E-01	9.05E-02	1 Unchanged Low
P36956	K10cd2	sterol regulatory element binding	140.2264	109	128.532	125.9988	-1.26E-01	-3.60E-01	1 Unchanged Low
P08236	D05ab3	glucuronidase; beta	123.7102	114	128.6103	122.0379	5.60E-02	-1.21E-01	1 Unchanged Low
Q13425	L12cd2	synrophin; beta 2 (dystrophin-as	106.7241	122	128.6723	119.2218	2.70E-01	1.98E-01	1 Unchanged Low
Q14676	E18gh1	KIAA0170 gene product	93.41268	145	128.7328	122.2375	4.63E-01	6.30E-01	1 Unchanged Low
P16106	O12gh6	H3 histone family; member F	98.02235	138	128.7695	120.7804	3.94E-01	4.66E-01	1 Unchanged Low
Q14773	J03ab6	Intercellular adhesion molecule 4	101.185	137	128.8098	122.4247	3.39E-01	4.24E-01	1 Unchanged Low
Q14736	N19gh4	putative methyltransferase	124.8741	126	128.8151	126.6152	4.48E-02	1.47E-02	1 Unchanged Low
Q9Y297	N21cd4	beta-transducin repeat containing	152.2664	142	128.8641	141.0555	-2.41E-01	-1.01E-01	1 Unchanged Low
Q13585	H16cd4	G protein-coupled receptor 50	121.9424	113	128.8853	121.1757	7.99E-02	-1.14E-01	1 Unchanged Low
O60858	L24cd5	ret finger protein 2	110.1643	110	128.8939	116.2529	2.27E-01	-6.09E-03	1 Unchanged Low
Q9V2Z6	E06ef2	CG1-07 protein	96.22816	139	128.9272	121.3443	4.22E-01	5.29E-01	1 Unchanged Low
Q9UG66	P16ef7	hypothetical protein DKFZp586G	318.3297	374	128.9795	273.7118	-1.30E+00	2.32E-01	1 Unchanged Low
Q9Y6G5	N17ef2	PTD002 protein	107.7937	141	129.1324	125.8408	2.61E-01	3.83E-01	1 Unchanged Low
P58155	E06cd3	very low density lipoprotein receptor	113.1365	104	129.1355	115.483	1.91E-01	-1.19E-01	1 Unchanged Low
Q9NP50	C07gh5	TERA protein	94.63638	199	129.2792	140.8474	4.50E-01	1.07E+00	1 Unchanged Low
P28328	C01ab8	peroxisomal membrane protein 3	321.6292	219	129.3474	223.2274	-1.31E+00	-5.56E-01	1 Unchanged Low
Q969T4	M24cd6	ubiquitin-conjugating enzyme E2	117.2071	100	129.3512	115.6428	1.42E-01	-2.24E-01	1 Unchanged Low
P19827	D18ab6	inter-alpha (globulin) inhibitor; H-	239.4455	186	129.3613	185.0551	-8.88E-01	-3.62E-01	1 Unchanged Low
O15096	M18ab8	phosphatidylinositol 4-kinase; ca	117.2574	115	129.4365	120.4316	1.43E-01	-3.31E-02	1 Unchanged Low

Q9Y5J6	J16cd7	fracture callus 1 homolog (rat)	102.357	127	129.4503	119.4401	3.39E-01	3.06E-01	1 Unchanged Low
Q92889	M24ab4	excision repair cross-complemen	157.5735	97.6	129.5255	128.238	-2.83E-01	-6.91E-01	1 Unchanged Low
P08697	C07ef1	serine (or cysteine) proteinase In	139.5253	136	129.5425	134.8048	-9.67E-02	-2.29E-02	1 Unchanged Low
Q9UBX1	A05cd4	cathepsin F	113.4065	118	129.6557	120.4495	1.93E-01	6.08E-02	1 Unchanged Low
Q9NP17	D22ef1	hypothetical protein LOC51315	240.5378	171	129.76	180.4148	-8.90E-01	-4.93E-01	1 Unchanged Low
P11586	D14ef7	methylenetetrahydrofolate dehyd	141.2456	106	129.8444	125.7751	-1.21E-01	-4.11E-01	1 Unchanged Low
Q96010	J15cd4	LIM domain binding 1	90.9506	155	129.8567	125.1912	5.14E-01	7.67E-01	1 Unchanged Low
Q13188	P13cd2	serine/threonine kinase 3 (STE21	117.4664	135	129.8809	127.4091	1.45E-01	1.99E-01	1 Unchanged Low
Q13845	I21ab3	B-cell CLL/lymphoma 7B	145.9359	68.3	129.9273	121.3988	-1.68E-01	-7.24E-01	1 Unchanged Low
Q9Y5W9	D07cd8	sorting nexin 11	144.6605	198	130.0152	157.7018	-1.54E-01	4.56E-01	1 Unchanged Low
O60539	I02cd7	Ras association (Raf/GDS/AF-1)	126.8466	102	130.0346	119.7412	3.58E-02	-3.10E-01	1 Unchanged Low
O60885	I02ef3	bromodomain-containing 4	114.9928	98.1	130.1093	114.4111	1.78E-01	-2.29E-01	1 Unchanged Low
Q9H2B0	O16gh5	nucleosome assembly protein 1-4	122.5782	147	130.1112	133.1825	8.60E-02	2.61E-01	1 Unchanged Low
P51582	C24ab4	pyrimidinergic receptor P2Y; G-p	116.4263	109	130.158	118.649	1.61E-01	-9.03E-02	1 Unchanged Low
O09585	F08cd1	small inducible cytokine subfamily	168.745	216	130.1849	171.5056	-3.74E-01	3.53E-01	1 Unchanged Low
Q15131	B23ef5	cyclin-dependent kinase (CDC24	168.6104	108	130.2201	135.7223	-3.73E-01	-6.38E-01	1 Unchanged Low
O75148	F08cd8	cryptochrom 2 (photolyase-like)	66.14249	172	130.27	129.5265	5.97E-01	9.99E-01	1 Unchanged Low
Q15691	G17cd8	microtubule-associated protein; F	173.7024	168	130.2758	157.4437	-4.15E-01	-4.51E-02	1 Unchanged Low
Q15779	H21ab8	procollagen (type III) N-endopept	141.4408	133	130.2905	135.0227	-1.18E-01	-8.51E-02	1 Unchanged Low
Q9UHD2	K14cd8	TANK-binding kinase 1	82.31867	172	130.2947	128.1679	6.62E-01	1.06E+00	1 Unchanged Low
Q9NSS3	K15gh3	hypothetical protein DKFZp434E	107.5389	115	130.3095	117.5518	2.77E-01	9.44E-02	1 Unchanged Low
Q13797	I01ef7	Integrin; alpha 9	156.9946	85	130.4752	124.1726	-2.67E-01	-8.84E-01	1 Unchanged Low
P46531	M10ef5	Notch homolog 1; translocation-e	86.01963	164	130.4897	126.8111	6.01E-01	9.30E-01	1 Unchanged Low
O43262	C01cd6	deleted in lymphocytic leukemia;	76.79463	195	130.4943	134.2594	7.65E-01	1.35E+00	1 Unchanged Low
Q9Y2H6	K12ef8	KIAA0970 protein	170.8655	128	130.5238	142.9858	-3.89E-01	-4.22E-01	1 Unchanged Low
P25768	J11ab8	proteasome (prosome; macropali	258.6025	285	130.5899	224.7239	-9.86E-01	1.40E-01	1 Unchanged Low
Q9BQ58	D09gh7	FYVE and coiled-coil domain cor	164.6348	207	130.6451	167.5571	-3.34E-01	3.33E-01	1 Unchanged Low
Q9Y396	J04ef1	elongation of very long chain fat	162.6431	82.2	130.6722	125.1558	-3.16E-01	-9.85E-01	1 Unchanged Low
Q9P0R7	K06ef2	hypothetical protein LOC51242	126.7302	218	130.6804	158.5209	4.43E-02	7.84E-01	1 Unchanged Low
O15269	F17cd6	serine palmitoyltransferase; long	97.42808	133	130.7429	120.3129	4.24E-01	4.46E-01	1 Unchanged Low
Q9UFX0	B02ef2	calcium binding atopy-related aar	233.5089	287	130.8943	217.1357	-8.35E-01	2.98E-01	1 Unchanged Low
Q9H663	F24gh5	likely ortholog of mouse actin-rel	98.1679	128	130.9258	119.1693	4.15E-01	-3.87E-01	1 Unchanged Low
Q75140	P17cd2	transforming; acidic coiled-coil $\alpha$	224.1188	133	130.9827	162.703	-7.75E-01	-7.53E-01	1 Unchanged Low
Q9Y5N5	I14cd8	putative N6-DNA-methyltransfera	99.34841	133	131.0924	121.2285	4.00E-01	4.24E-01	1 Unchanged Low
Q9BQ72	F02gh7	hypothetical protein MGCG10471	106.3824	115	131.1126	117.4135	3.02E-01	1.09E-01	1 Unchanged Low
Q9Y303	E10ef2	CGI-14 protein	153.5787	101	131.2035	128.5162	-2.27E-01	-6.08E-01	1 Unchanged Low
Q9P005	A22ef8	HSPC159 protein	341.3083	579	131.3146	350.7027	-1.38E+00	7.64E-01	1 Unchanged Low
Q9Y3A1	H19ef2	DKFZP566004 protein	200.4927	262	131.3154	198.1031	-6.08E-01	3.88E-01	1 Unchanged Low
Q15172	C12cd1	protein phosphatase 2; regulator	168.3914	140	131.5524	146.553	-3.56E-01	-2.69E-01	1 Unchanged Low
Q9BV19	I19gh6	hypothetical protein MGCG55	96.47316	141	131.6168	122.8739	4.48E-01	5.43E-01	1 Unchanged Low
Q14534	E11cd2	squalene epoxidase	155.5799	71.3	131.8107	119.574	-2.39E-01	-1.13E+00	1 Unchanged Low
Q9BS43	G19gh8	hypothetical protein MGCG12435	592.1694	121	131.9022	281.8569	-2.17E-01	-2.29E+00	1 Unchanged Low
P49788	D24ab8	retinol acid receptor responder	97.19637	135	131.9355	121.3412	4.41E-01	4.73E-01	1 Unchanged Low
Q9UP83	M10cd6	component of oligomeric golgi cc	100.2446	141	131.9356	124.3058	3.96E-01	4.89E-01	1 Unchanged Low
Q9Y2X0	N11cd5	thyroid hormone receptor-associat	116.8892	97.9	131.9541	115.5741	1.75E-01	-2.56E-01	1 Unchanged Low
Q9Y3E3	I15ef2	CGI-145 protein	94.76733	132	131.9919	119.5355	4.78E-01	4.76E-01	1 Unchanged Low
O95183	J14cd6	vesicle-associated membrane pn	91.19765	157	132.0539	126.6473	5.34E-01	7.81E-01	1 Unchanged Low
Q13242	N22cd3	splice factor; arginine/serine-ri	156.0624	141	132.0637	143.0016	-2.41E-01	-1.48E-01	1 Unchanged Low
Q9Y5R5	A06gh1	doublesex and mab-3 related trai	100.8446	162	132.1528	131.5571	3.90E-01	6.81E-01	1 Unchanged Low
P04181	N02ab7	ornithine aminotransferase (gyr)	112.3954	106	132.1687	116.724	2.34E-01	-8.99E-02	1 Unchanged Low
Q14254	B15ab7	flotillin 2	130.1586	154	132.2038	138.6301	2.25E-02	2.38E-01	1 Unchanged Low
Q9Y6E6	P08cd7	sirtuin silent mating type Informa	94.40989	136	132.2501	121.0265	4.86E-01	5.31E-01	1 Unchanged Low
Q9H237	D20gh5	porcupine	148.2204	258	132.2656	179.3923	-1.64E-01	7.98E-01	1 Unchanged Low
Q92785	N21cd2	requiem; apoptosis response zin	118.3718	108	132.3893	119.5733	1.61E-01	-1.26E-01	1 Unchanged Low
O95458	N11cd2	tubulin- $\beta$ -specific chaperone d	128.9522	100	132.4761	120.4814	3.89E-02	-3.67E-01	1 Unchanged Low
P20749	P23ef6	B-cell CLL/lymphoma 3	264.1174	186	132.484	194.2507	-9.95E-01	-5.05E-01	1 Unchanged Low
Q9H2N8	D24gh7	hypothetical protein GL012	104.3233	160	132.5197	132.1507	3.45E-01	6.14E-01	1 Unchanged Low
Q15020	M08gh1	squamous cell carcinoma antigen	117.2757	147	132.5393	132.2727	1.77E-01	3.26E-01	1 Unchanged Low
P42025	O01gh1	ARP1 actin-related protein 1 hor	243.7979	92	132.554	156.1129	-8.79E-01	-1.41E+00	1 Unchanged Low
P98173	I23gh5	2.19 gene	113.0426	116	132.6703	120.727	2.31E-01	4.31E-02	1 Unchanged Low
Q95295	C06cd8	SNARE associated protein snapl	324.3312	119	132.6986	192.0882	-1.29E+00	-1.44E+00	1 Unchanged Low
Q9NV1A	F15gh3	chromosome 20 open reading frz	111.7508	100	132.7232	114.8529	2.48E-01	-1.59E-01	1 Unchanged Low
P35573	O03ab2	amyo-1; 6-glucosidase; 4-alpha-	111.9563	106	132.7432	116.8065	2.46E-01	-8.27E-02	1 Unchanged Low
Q13126	K13ab7	methylthioadenosine phosphoryl	202.8169	236	132.9211	190.4847	-6.10E-01	2.17E-01	1 Unchanged Low
P43034	C11ab8	platelet-activating factor acetylhy	106.8174	125	132.987	121.4511	3.16E-01	2.22E-01	1 Unchanged Low
Q01844	E15ab5	Ewing sarcoma breakpoint region	111.2628	102	133.001	115.5021	2.57E-01	-1.22E-01	1 Unchanged Low
P27482	E18ab6	calmodulin-like 3	114.7017	104	133.018	117.2725	2.14E-01	-1.40E-01	1 Unchanged Low
Q9NIUW4	N23gh3	BRIX	223.8591	77.1	133.0208	144.6673	-7.51E-01	-1.54E+00	1 Unchanged Low
P78552	J23ab6	interleukin 13 receptor; alpha 1	118.2476	93.9	133.0765	115.0749	1.70E-01	-3.33E-01	1 Unchanged Low
P51643	O24ab4	nuclear receptor subfamily 0; gro	104.7329	112	133.1401	116.7757	3.46E-01	1.03E-01	1 Unchanged Low
P15822	L23ab5	human immunodeficiency virus t	83.26942	160	133.2118	125.3978	6.78E-01	9.40E-01	1 Unchanged Low
Q9BXV9	O13gh8	RALBP1 associated Eps domain	90.84238	140	133.2741	121.2561	5.53E-01	6.20E-01	1 Unchanged Low
Q9ULB4	P10ef1	cadherin 9; type 2 (T1-cadherin)	275.2974	137	133.4641	181.8847	-1.04E+00	-1.01E+00	1 Unchanged Low
Q9NZZ7	C06ef8	HSPC171 protein	214.9523	265	133.5412	204.594	-6.87E-01	3.04E-01	1 Unchanged Low
Q02086	C09cd2	Sp2 transcription factor	101.0989	133	133.5465	122.3826	4.02E-01	3.90E-01	1 Unchanged Low
Q9BUV9	H14gh8	DKFZP586J0119 protein	102.1174	119	133.5923	118.2651	3.88E-01	2.22E-01	1 Unchanged Low
Q9UHJ9	A09ef4	FGF receptor activating protein 1	100.7903	121	133.6008	118.5627	4.07E-01	2.67E-01	1 Unchanged Low
Q16401	E11cd1	proteasome (prosome; macropali	143.6091	120	133.6156	132.2946	-1.04E-01	-2.63E-01	1 Unchanged Low
Q9Y4K4	D04cd6	mitogen-activated protein kinase	132.4072	158	133.6676	141.2069	1.37E-02	2.51E-01	1 Unchanged Low
O60463	H06cd3	phosphatidic acid phosphatase I	103.2417	151	133.6898	129.2479	3.73E-01	5.47E-01	1 Unchanged Low
Q95639	P26cd6	cleavage and polyadenylation sp	183.1762	67.6	133.7241	128.1539	-4.54E-01	-1.44E+00	1 Unchanged Low
P50539	N19ab7	MAX interacting protein 1	175.6646	187	133.7304	165.4016	-3.93E-01	8.87E-02	1 Unchanged Low
Q9UH52	I15ef3	ALEX3 protein	118.2527	171	133.7314	140.9912	1.77E-01	5.32E-01	1 Unchanged Low
O15525	C13ab7	v-maf musculoaponeurotic fibros	105.3252	109	133.7521	116.1167	3.45E-01	5.31E-02	1 Unchanged Low
Q9H8T0	H21gh5	fused toes homolog (mouse)	106.2145	241	133.7606	160.2791	3.33E-01	1.18E+00	1 Unchanged Low
Q9Y4X5	K03cd6	arafadin homolog; ubiquitin-conju	99.46477	128	133.8771	120.4976	4.29E-01	3.66E-01	1 Unchanged Low

Q9H9E1	O01gh5	ankyrin repeat; family A (RFXAN	172.6266	78.8	134.052	128.4841	-3.65E-01	-1.13E+00	1	Unchanged	Low
Q93063	F13ab3	exosloses (multiple) 2	123.2886	181	134.3466	139.4501	1.24E-01	3.82E-01	1	Unchanged	Low
Q9H992	D22gh5	axotrophin	89.54768	149	134.4784	124.4411	5.87E-01	7.37E-01	1	Unchanged	Low
O43237	P02ab4	dynel; cytoplasmic; light interme	290.6769	119	134.4914	181.4903	-1.11E+00	-1.28E+00	1	Unchanged	Low
Q99643	H02cd1	succinate dehydrogenase comp1	143.4474	125	134.5527	134.443	-9.24E-02	-1.95E-01	1	Unchanged	Low
P24386	F11ef1	choroideromla (Rab escort prot)	93.86058	129	134.5533	119.0446	5.20E-01	4.58E-01	1	Unchanged	Low
Q9Y5F7	F12gh4	protocadherin gamma subfamily	101.7878	114	134.5585	116.632	4.03E-01	1.58E-01	1	Unchanged	Low
P06756	D14ab5	integrin; alpha V (vitronectin rec)	200.0782	219	134.6115	184.6891	-5.72E-01	1.33E-01	1	Unchanged	Low
Q9HS57	C02gh6	chromosome 1 open reading frar	173.8108	148	134.6601	152.0822	-3.68E-01	-2.34E-01	1	Unchanged	Low
O15517	A14ef8	tumor necrosis factor receptor su	82.33364	207	134.6603	144.7566	5.44E-01	1.17E+00	1	Unchanged	Low
Q9PON5	K24ef2	HSPC244	107.9991	129	134.6618	123.7732	3.18E-01	2.53E-01	1	Unchanged	Low
Q9NWT2	D19gh2	hypothetical protein FLJ20623	107.8864	105	134.7112	115.8334	3.20E-01	-4.05E-02	1	Unchanged	Low
Q9Y2A0	O02cd7	TP53 target gene 1	127.408	88.2	134.8491	116.8334	8.19E-02	-5.30E-01	1	Unchanged	Low
Q9NZ43	N16gh4	uncharacterized-hemopoietic si	141.2528	137	134.8524	137.7883	-6.58E-01	-4.24E-02	1	Unchanged	Low
P27986	A10ef1	phosphoinositide-3-kinase; regul	111.3806	112	134.9588	119.3503	2.77E-01	4.28E-03	1	Unchanged	Low
Q9UBP6	J13ef1	methyltransferase-like 1	107.2187	122	134.9886	121.358	3.32E-01	1.85E-01	1	Unchanged	Low
Q9BWK5	F24gh5	hypothetical protein MGC5242	101.1324	123	134.9881	119.8654	4.17E-01	2.88E-01	1	Unchanged	Low
P54802	M24ab6	N-acetylglucosaminidase; alpha-	206.038	66.3	135.077	135.7965	-6.09E-01	-1.64E+00	1	Unchanged	Low
Q75953	H09cd7	G-protein coupled receptor	110.3886	184	135.3412	143.3711	2.94E-01	7.40E-01	1	Unchanged	Low
Q9NZ24	F03ef4	TLG protein	124.5205	105	135.3934	121.5448	1.21E-01	-2.50E-01	1	Unchanged	Low
O60353	B11cd3	frizzled homolog 6 (Drosophila)	85.84918	146	135.5169	122.5147	6.62E-01	7.73E-01	1	Unchanged	Low
Q9NQS6	F13gh4	latexin protein	94.21822	163	135.5761	130.917	5.25E-01	7.90E-01	1	Unchanged	Low
O14776	A19cd7	transcription elongation regulator	113.3803	117	135.6603	122.1137	2.59E-01	4.90E-02	1	Unchanged	Low
Q9VS42	L13ef1	putative zinc finger protein NY-R	154.0704	186	135.6708	158.5684	-1.83E-01	2.71E-01	1	Unchanged	Low
P49842	G23cd6	serine/threonine kinase 19	133.3557	171	135.7013	146.5953	2.52E-02	3.56E-01	1	Unchanged	Low
Q06546	J14ab5	GA binding protein transcription	88.93312	138	135.7488	120.885	6.10E-01	6.34E-01	1	Unchanged	Low
Q9Y2E7	I02ef2	KIAA0938 protein	109.8218	105	135.7763	116.739	3.06E-01	-7.00E-02	1	Unchanged	Low
Q9UM11	I02ef2	Zf1 protein	80.82847	186	135.8849	134.12	7.50E-01	1.20E+00	1	Unchanged	Low
Q99447	B14ab8	phosphate cytidylyltransferase 2;	174.8201	77.4	135.988	129.39	-3.62E-01	-1.18E+00	1	Unchanged	Low
Q9H1R3	F22gh8	myosin light chain kinase 2; skele	93.58977	129	136.0456	119.5324	5.40E-01	4.63E-01	1	Unchanged	Low
P28358	P05ab6	homeobox D10	108.9905	102	136.1419	115.6766	3.21E-01	-9.71E-02	1	Unchanged	Low
O76070	P18cd1	synuclein; gamma (breast cancer)	128.551	140	136.1645	134.744	8.30E-02	1.18E-01	1	Unchanged	Low
Q9Y5A7	N07ef2	NEDD8 ultimate buster-1	119.0653	195	136.2605	149.951	1.95E-01	7.08E-01	1	Unchanged	Low
Q9NWY7	A16gh3	hypothetical protein FLJ20530	103.7638	110	136.3026	116.6328	3.94E-01	8.20E-02	1	Unchanged	Low
O43715	P02ef2	hypothetical protein HSPC132	137.4694	110	136.3043	127.9562	-1.23E-02	-3.20E-01	1	Unchanged	Low
Q9BV75	K19gh8	itchy homolog E3 ubiquitin prote	118.5721	127	136.5094	127.3323	2.03E-01	9.81E-02	1	Unchanged	Low
O43431	A12ef7	endothelial differentiation; lysop	126.4659	171	136.5393	144.6131	1.11E-01	4.34E-01	1	Unchanged	Low
O43567	D15cd7	rigid finger protein 13	110.4449	153	136.5722	133.3964	3.06E-01	4.72E-01	1	Unchanged	Low
Q9Y2Z7	P13ef8	DKFZP586F1524 protein	113.1366	104	136.7041	117.8414	2.73E-01	-1.26E-01	1	Unchanged	Low
O14582	O24ef2	spondyloepiphyseal dysplasia; Ia	135.1666	135	136.7342	135.7349	1.66E-02	1.46E-03	1	Unchanged	Low
O75056	G12gh1	syndecan 3 (N-syndecan)	120.0661	162	136.797	139.5562	1.88E-01	4.31E-01	1	Unchanged	Low
Q9PZY2	D18gh4	b1a:14 mannosyltransferase	89.6857	143	136.8208	123.2251	6.09E-01	6.75E-01	1	Unchanged	Low
Q16595	M08ab3	Friedreich ataxia	139.5657	130	136.8314	135.5917	-2.65E-02	-9.82E-02	1	Unchanged	Low
Q14807	B18ab7	kinesin-like 4	114.4726	94.2	136.9298	115.2048	2.58E-01	-2.81E-01	1	Unchanged	Low
Q9BZL4	L10gh6	protein phosphatase 1; regulator	110.5367	123	137.0777	123.5234	3.10E-01	1.54E-01	1	Unchanged	Low
P30876	I13ab8	polymerase (RNA) II (DNA direc	265.5337	200	137.1153	200.7168	-9.54E-01	-4.12E-01	1	Unchanged	Low
Q9UGP6	B17cd7	cotainer protein complex; subar	94.73601	134	137.2091	122.0845	5.35E-01	5.02E-01	1	Unchanged	Low
P52655	M01ef2	general transcription factor IIa; I	121.4896	128	137.3707	129.1154	1.77E-01	8.08E-02	1	Unchanged	Low
Q9HB07	G23gh5	chromosome 12 open reading fra	121.2547	118	137.4723	125.5248	1.81E-01	-4.11E-02	1	Unchanged	Low
Q92940	H23ab7	MAD; mothers against decapent	414.4889	223	137.6028	258.3032	-1.59E-00	-9.95E-01	1	Unchanged	Low
Q9NWV1	H19gh2	hypothetical protein FLJ20727	117.7514	120	137.6351	124.9938	2.25E-01	2.24E-02	1	Unchanged	Low
O43664	A10cd6	G protein-coupled receptor 66	108.1311	102	137.6789	116.0604	3.49E-01	-7.90E-02	1	Unchanged	Low
O14647	C19ab4	chromodomain helicase DNA bin	96.14904	164	137.7441	132.5407	5.19E-01	7.58E-01	1	Unchanged	Low
O75333	N15cd2	T-box 10	126.0065	129	137.7737	130.9257	1.29E-01	3.38E-02	1	Unchanged	Low
Q16539	J04ef5	mitogen-activated protein kinase	148.7339	219	137.8	168.4312	-1.10E-01	5.57E-01	1	Unchanged	Low
Q9NOG5	A07gh5	chromosome 20 open reading fra	86.80552	143	137.803	122.4598	6.67E-01	7.18E-01	1	Unchanged	Low
Q15149	E05ab8	pectin 1; intermediate filament bi	125.7248	83.9	138.0765	115.8848	1.35E-01	-5.84E-01	1	Unchanged	Low
Q9NVZ7	G12gh3	hypothetical protein FLJ10407	166.213	175	138.1444	159.6342	-2.67E-01	7.06E-02	1	Unchanged	Low
Q15800	D02cd2	sterol-C4-methyl oxidase-like	171.8648	71.2	138.1497	127.0641	-3.15E-01	-1.27E+00	1	Unchanged	Low
Q9H0B6	D16gh5	hypothetical protein FLJ12387 si	95.54943	129	138.1542	121.3672	5.17E-01	4.22E-01	1	Unchanged	Low
P09001	K14cd7	mitochondrial ribosomal protein l	94.17331	128	138.1601	120.1502	5.53E-01	4.44E-01	1	Unchanged	Low
O00301	D24cd3	KH-type splicing regulatory prote	126.0509	88.3	138.3014	117.5428	1.34E-01	-5.14E-01	1	Unchanged	Low
P55785	J19ef7	aminopeptidase purinyl sensi	273.7328	98.9	138.3924	170.346	-9.84E-01	-1.47E+00	1	Unchanged	Low
Q9Y5Y9	B14cd2	sodium channel; voltage-gated; t	127.3727	139	138.4331	134.9928	1.20E-01	1.28E-01	1	Unchanged	Low
P19235	M01ef7	erythropoletin receptor	198.5954	77.3	138.4803	138.1099	-5.20E-01	-1.36E+00	1	Unchanged	Low
O15228	A16ef3	glycerophosphocholine O-acyltrans	225.1315	186	138.5137	163.349	-7.01E-01	-2.72E+01	1	Unchanged	Low
Q9UK97	K05cd8	F-box only protein 9	151.0501	104	138.5593	131.097	-1.25E-01	-5.43E-01	1	Unchanged	Low
P50990	D20cd6	chaperonin containing TCP-1; sut	274.982	178	138.6001	197.1593	9.88E-01	6.28E-01	1	Unchanged	Low
Q9NZM1	P19cd8	ferritin-like 3; myoferritin (C. elegan	218.8411	202	138.6209	166.4122	-6.59E-01	-1.17E-01	1	Unchanged	Low
Q92924	N20cd1	SWI/SNF related; matrix associat	131.7669	82.7	138.6764	117.704	7.37E-01	-6.73E-01	1	Unchanged	Low
Q75845	A18gh1	sterol-C5-desaturase (ERG3 dell	101.9285	153	138.7232	131.1196	4.45E-01	5.83E-01	1	Unchanged	Low
Q9NQ88	I10gh4	chromosome 12 open reading fra	80.2401	158	138.8274	125.605	7.91E-01	9.75E-01	1	Unchanged	Low
Q16515	C19ab2	amifpride-sensitive cation chan	102.1159	109	138.9915	116.6136	4.45E-01	9.06E-02	1	Unchanged	Low
P49759	F16ab5	CDC-like kinase 1	85.24615	147	139.0985	124.2553	6.90E-01	7.73E-01	1	Unchanged	Low
P33552	A22ab5	CDC28 protein kinase 2	109.5671	96	139.1297	114.8881	3.45E-01	-1.91E-01	1	Unchanged	Low
Q75808	H21cd2	small optic lobes homolog (Dros	115.654	98.9	139.1625	117.8698	2.67E-01	-2.26E-01	1	Unchanged	Low
Q9NXR1	M07gh2	LIS1-interacting protein NUDE1;	96.20481	123	139.1939	119.5057	5.33E-01	3.56E-01	1	Unchanged	Low
Q75381	L12ab8	peroxisomal biogenesis factor 14	473.8395	113	139.2209	241.8793	-1.77E+00	-2.07E+00	1	Unchanged	Low
O60930	P23cd1	ribonuclease H1	167.3611	111	139.2393	139.1464	-2.65E-01	-5.95E-01	1	Unchanged	Low
O14653	P14cd4	golgi SNAP receptor complex me	115.7917	89.7	139.2541	114.9152	2.66E-01	-3.68E-01	1	Unchanged	Low
Q16540	L24gh1	mitochondrial ribosomal protein l	209.2433	120	139.3426	156.1365	-5.87E-01	-8.04E-01	1	Unchanged	Low
O14658	P08cd2	ras-related Cx botulinum toxin st	158.176	166	139.3634	154.6374	-1.83E-01	7.29E-02	1	Unchanged	Low
Q15814	M17cd2	tubulin-specific chaperone c	103.3699	112	139.5311	118.2869	4.34E-01	1.14E-01	1	Unchanged	Low
Q9Y3C9	J09ef2	CG1-127 protein	83.4762	163	139.6599	128.8568	7.42E-01	9.69E-01	1	Unchanged	Low
P18827	F22cd1	syndecan 1	114.4045	92.7	139.6607	115.5895	2.88E-01	-3.03E-01	1	Unchanged	Low
P04450	B21ab3										

Q9Y301	N05ef1	CGI-12 protein	108.0511	101	139.7035	116.3594	3.71E-01	-9.27E-02	1	Unchanged Low	
O00626	F10cd1	small inducible cytokine subfamily	113.478	106	139.8189	119.8588	3.01E-01	-8.45E-02	1	Unchanged Low	
B18cd8		neural precursor cell expressed;	108.1711	133	139.9597	127.048	3.72E-01	-2.98E-01	1	Unchanged Low	
Q9Y311	C01ef2	mitochondrial ribosomal protein l	162.6519	74.8	139.9856	125.8788	-2.18E-01	-1.12E+00	1	Unchanged Low	
Q15633	K14cd2	TAR (HIV) RNA binding protein 2	169.3779	125	140.0138	144.9588	-2.75E-01	-4.33E-01	1	Unchanged Low	
P02278	M22gh6	H2B histone family; member K	100.2794	216	140.0965	152.2309	4.82E-01	1.11E+00	1	Unchanged Low	
PS3672	J11cd7	crystallin; beta A2	101.7321	187	140.2804	142.8494	4.64E-01	8.75E-01	1	Unchanged Low	
P09417	C05ab8	quinoid dihydroperoxide reductase	126.6361	161	140.3564	142.5395	1.48E-01	3.43E-01	1	Unchanged Low	
Q9HYA2	K14gh5	MAGEF1 protein	96.01675	126	140.3554	120.9341	5.48E-01	3.97E-01	1	Unchanged Low	
P30273	A20cb5	Fc fragment of IgE; high affinity I	88.48289	171	140.4541	133.3475	6.67E-01	9.51E-01	1	Unchanged Low	
Q9Z978	G10ab4	forkhead box J1	250.4112	167	140.5084	185.89	-8.34E-01	-5.87E-01	1	Unchanged Low	
Q9GZT9	G10gh7	elegine homolog 1 (C. elegans)	112.8025	99.2	140.6556	117.5626	3.18E-01	-1.85E-01	1	Unchanged Low	
P35658	O23cd4	nucleoplasm 214KD (CAIN)	141.8279	137	140.7761	139.8811	-1.07E-02	-4.96E-02	1	Unchanged Low	
Q9HB40	G01gh5	likely homolog of rat and mouse	105.9316	99.3	140.9548	115.3964	4.12E-01	-9.32E-02	1	Unchanged Low	
O14586	O16cd3	myeloid/lymphoid or mixed-lineage	117.844	157	141.0674	138.5398	2.60E-01	4.11E-01	1	Unchanged Low	
Q92911	O12cd1	solute carrier family 5 (sodium ion)	264.1256	125	141.0904	176.594	-9.05E-01	-1.08E+00	1	Unchanged Low	
Q9Y5E4	B18ef3	protocadherin beta 5	95.08061	148	141.1894	127.9379	5.70E-01	6.34E-01	1	Unchanged Low	
Q13057	H17gh7	nucleotide binding protein	186.8796	125	141.2202	151.0906	-4.04E-01	-5.78E-01	1	Unchanged Low	
Q14863	K23ab8	POU domain; class 6; transcription	103.2077	103	141.3258	115.7954	4.53E-01	-4.97E-03	1	Unchanged Low	
P36610	G10ef3	frequenin homolog (Drosophila)	110.2191	136	141.4925	129.0874	3.60E-01	2.98E-01	1	Unchanged Low	
O60240	O12ab8	perilipin	112.1108	52.2	141.5046	438.2653	-2.99E+00	-4.43E+00	1	Unchanged Low	
Q9H984	P05gh5	hypothetical protein FLJ12876	87.99841	133	141.7125	120.8973	6.87E-01	5.96E-01	1	Unchanged Low	
O00584	J14cd3	ribonuclease 6 precursor	124.6932	250	141.8008	172.0542	1.85E-01	1.00E+00	1	Unchanged Low	
Q9H658	M04gh7	G protein-coupled receptor 107	158.2595	214	141.8139	171.1973	-1.58E-01	4.32E-01	1	Unchanged Low	
P18858	K14ef6	ligase I; DNA: ATP-dependent	92.33071	128	141.8761	120.8853	6.20E-01	4.76E-01	1	Unchanged Low	
Q9HAR6	O10gh5	leukemia inhibitory factor (cholin)	253.8099	297	141.8885	295.8854	-1.66E+00	-5.99E-01	1	Unchanged Low	
P15018	O18ef7	D23cd1	ribosomal protein L26	449.1728	119	141.9661	174.2861	-8.81E-01	-1.13E+00	1	Unchanged Low
Q13546	A23cd4	glucosamine (N-acetyl)-6-sulfatase	261.466	231	141.9948	161.4649	3.56E-01	1.06E+00	1	Unchanged Low	
P24298	H01ab4	KIAA0117 protein	110.9202	101	142.0352	116.2449	4.32E-01	-5.47E-02	1	Unchanged Low	
Q14129	C22cd4	molybdenum cofactor synthesis	105.3087	214	142.0643	183.3737	-4.48E-01	1.45E-01	1	Unchanged Low	
Q9BQAZ	K09gh8	Fancn anemia; complement-like	193.8104	198	142.0669	152.8734	2.56E-01	7.32E-01	1	Unchanged Low	
Q9UJX9	B12ef3	uterine-derived 14 kDa protein	118.9551	309	142.2733	235.0602	-8.35E-01	2.84E-01	1	Unchanged Low	
Q95950	I01cd5	splicing factor; estradiol-Ind	231.0328	131	142.2746	137.7012	2.63E-02	-9.15E-02	1	Unchanged Low	
O14798	C06ef7	receptor (TNFRSF)-Interacting si	139.7074	97.1	142.3123	149.9584	-5.64E-01	-1.12E+00	1	Unchanged Low	
P32238	P01ab3	glutamic-pyruvate transaminase	210.426	141	142.4302	131.8973	3.45E-01	3.32E-01	1	Unchanged Low	
Q9UQ90	C17cd2	DIGeorge syndrome critical regio	112.1253	187	142.4325	164.7437	-2.12E-01	1.80E-01	1	Unchanged Low	
P82980	M03gh8	KIAA1882 protein	164.9357	98.5	142.5053	120.9085	2.27E-01	-3.06E-01	1	Unchanged Low	
P49716	P15ab5	hypothetical protein; estradiol-Ind	121.7396	199	142.5273	190.7413	-6.97E-01	-2.18E-01	1	Unchanged Low	
P20062	M12cd1	splice factor; arginine/serine-rich	231.0328	213	142.5294	166.073	-1.68E-03	5.78E-01	1	Unchanged Low	
P21580	B06cd2	tumor necrosis factor; alpha-Indu	275.8225	173	143.1867	170.7835	-4.52E-01	-1.76E-01	1	Unchanged Low	
Q99774	H01cd5	protein phosphatase 4; regulator	195.85	101	143.2517	116.1881	-5.00E-02	5.00E-02	1	Unchanged Low	
Q9P071	A17ef3	hypothetical protein HSPC192	104.4363	139	143.2732	122.6343	7.51E-01	7.12E-01	1	Unchanged Low	
P06737	B18ab8	phosphorylase; glycogen; liver (t	85.14818	144	143.2945	145.705	-6.52E-02	-5.91E-02	1	Unchanged Low	
O15063	K10gh1	KIAA0355 gene product	149.9191	94.7	143.3031	115.3343	4.08E-01	-1.90E-01	1	Unchanged Low	
P02743	K14ab2	amyloid P component; serum	108.0152	109	143.3056	129.6057	7.10E-02	-3.23E-01	1	Unchanged Low	
Q9NVTO	I14gh3	hypothetical protein FLJ10534	136.4264	104	143.4853	119.7013	3.56E-01	-1.14E-01	1	Unchanged Low	
Q9Y4P3	O07ef3	transducin (beta)-like 2	112.0852	88.7	143.5269	265.9537	-1.77E+00	-1.54E+00	1	Unchanged Low	
Q13888	N14ab3	basic transcription element binding	164.4049	106	143.5829	117.1232	4.96E-01	5.83E-02	1	Unchanged Low	
Q9NVPI8	L19gh4	hypothetical protein FLJ10595	101.7956	132	143.6823	144.5673	-1.40E-01	-2.66E-01	1	Unchanged Low	
P08240	G05cd2	signal recognition particle recept	158.3565	170	144.0988	176.2086	-3.24E-01	1.78E-01	1	Unchanged Low	
P49459	M19ef5	ubiquitin-conjugating enzyme E2	98.6462	169	144.1057	162.3327	-2.58E-01	-3.56E-02	1	Unchanged Low	
Q9NVA8	L16gh2	solute carrier family 38; member	112.6488	127	143.7695	127.9498	3.52E-01	1.78E-01	1	Unchanged Low	
P25325	K23cd3	mercaptoypyruvate sulfurtransferase	288.1435	274	143.8077	235.1972	-1.00E+00	-7.45E-02	1	Unchanged Low	
Q9UJH6	K08cd7	DEAD/H (Asp-Glu-Ala-Asp-His)t	135.6599	209	143.8383	162.7208	8.43E-02	6.21E-01	1	Unchanged Low	
P52298	H01cd7	nuclear cap binding protein subu	138.9223	191	143.8819	157.996	5.06E-02	4.61E-01	1	Unchanged Low	
Q9QN30	A10cd7	endothelial cell-specific molecule	104.1846	122	143.9703	123.2921	4.67E-01	2.24E-01	1	Unchanged Low	
O00541	I08ef3	pescadillo homolog 1; containing	180.43	204	144.0988	176.2086	-3.24E-01	1.78E-01	1	Unchanged Low	
Q9H2V9	B06gh7	hypothetical protein CDA08	173.5608	169	144.1057	162.3327	-2.58E-01	-3.56E-02	1	Unchanged Low	
Q9NNX1	F12gh1	tuftelin 1	147.0323	175	144.106	155.2599	-2.90E-02	2.49E-01	1	Unchanged Low	
Q13508	H14ab2	ADP-ribosyltransferase 3	109.4052	101	144.1545	118.095	3.98E-01	-1.19E-01	1	Unchanged Low	
Q9NR30	B21gh6	DEAD/H (Asp-Glu-Ala-Asp-His)t	110.4836	130	144.2348	128.2929	3.85E-01	2.36E-01	1	Unchanged Low	
Q14320	E15cd5	DNA segment on chromosome X	102.5057	178	144.2677	141.6929	4.93E-01	7.99E-01	1	Unchanged Low	
Q04726	D03cd2	transducin-like enhancer of split	211.8773	115	144.3217	156.9544	-5.54E-01	-8.66E-01	1	Unchanged Low	
P20061	N13cd1	transcobalamin I (Vitamin B12 bl	117.3445	85.5	144.4835	115.787	3.00E-01	-4.56E-01	1	Unchanged Low	
Q9Y21	J12ef2	polymerase (RNA) III (DNA direc	153.7426	145	144.5561	147.7222	-8.89E-02	-8.58E-02	1	Unchanged Low	
P35754	G22ab5	glutaredoxin (thioltransferase)	153.823	138	144.7308	145.4267	-8.79E-02	-1.59E-01	1	Unchanged Low	
Q02978	F01cd3	solute carrier family 25 (mitchond	106.877	98.2	144.7822	116.6268	4.38E-01	-1.22E-01	1	Unchanged Low	
Q95792	N20gh2	protein associated with PRK1	130.6914	146	144.7909	140.5872	1.48E-01	1.63E-01	1	Unchanged Low	
Q13232	D20ef7	non-melastatic cells 3; protein ex	90.7906	156	144.8861	130.592	6.74E-01	7.82E-01	1	Unchanged Low	
Q9NVH2	L01ef8	seven in sensilla homolog 2 (Dn	114.6318	91.2	144.9821	117.932	3.01E-01	-3.68E-01	1	Unchanged Low	
Q14331	G04ab5	DKFZP434B168 protein	117.6587	172	145.3307	183.8604	-6.89E-01	-4.46E-01	1	Unchanged Low	
Q15561	O15cd2	TEA domain family member 4	234.306	135	145.3321	130.2668	3.90E-01	2.78E-01	1	Unchanged Low	
Q9UPN9	B01ef2	tripartite motif-containing 33	110.9269	103	145.3798	119.1987	4.14E-01	-8.24E-02	1	Unchanged Low	
Q14353	O06ab3	guanidinoacetate N-methyltransf	109.1385	122	145.5587	139.1802	-4.40E-02	-3.01E-01	1	Unchanged Low	
Q9NZM5	A18ef4	glioma tumor suppressor candidate	150.098	101	145.653	120.4593	3.46E-01	-1.81E-01	1	Unchanged Low	
O43255	B11cd2	seven in sensilla homolog 2 (Dn	114.6318	176	145.6576	161.7607	-1.72E-01	9.77E-02	1	Unchanged Low	
Q14331	G04ab5	FSHD region gene 1	164.0964	154	145.6654	142.5299	1.92E-01	2.75E-01	1	Unchanged Low	
P18847	N23ab5	activating transcription factor 3	127.5442	223	145.6821	176.0472	-1.33E-01	4.79E-01	1	Unchanged Low	
O60258	I07cd4	fibroblast growth factor 17	159.7671	92.8	145.699	129.8767	-5.31E-02	-7.04E-01	1	Unchanged Low	
P47929	P02ab6	lectin; galactoside-binding; solub	151.1595	151	145.8554	135.0089	4.30E-01	4.80E-01	1	Unchanged Low	
P35227	O14cd4	zinc finger protein 144 (Me1-18)	108.2295	80.5	145.993	131.8082	-2.11E-01	-1.07E-01	1	Unchanged Low	
Q15599	O15cd5	solute carrier family 9 (sodium/h	168.9673								

Q9UKJ5	B20cd7	cystein-rich hydrophobic domain	164.4717	206	145.9967	178.8637	-3.37E-01	1.60E-01	1	Unchanged Low
Q9HC99	C10gh5	chromosome 1 open reading frar	94.16759	126	146.1583	122.1779	6.34E-01	4.22E-01	1	Unchanged Low
Q9Y3A0	K07er2	CGI-92 protein	119.1033	178	146.1698	147.7783	2.95E-01	5.80E-01	1	Unchanged Low
P49815	M17ef6	tuberous sclerosis 2	106.0159	163	146.2712	138.4231	4.64E-01	6.20E-01	1	Unchanged Low
P25116	L19ab4	coagulation factor II (thrombin) re	82.48228	143	146.2742	123.8585	8.27E-01	7.92E-01	1	Unchanged Low
Q75829	O01cd7	chondromodulin I precursor	121.7658	119	146.4976	128.9495	2.67E-01	3.81E-02	1	Unchanged Low
Q9NY11	M16ef2	ECSIT	111.7926	110	146.6345	122.8588	3.91E-01	-2.14E-02	1	Unchanged Low
P24347	I24ef5	matrix metalloproteinase 11 (stro	97.57916	136	146.6449	126.9018	5.88E-01	4.84E-01	1	Unchanged Low
O43189	K24ab8	PHD finger protein 1	112.1101	101	146.6325	120.038	3.88E-01	-1.46E-01	1	Unchanged Low
Q9P029	N22ef2	TH1-like (Drosophila)	201.2292	159	146.6998	168.9188	-4.56E-01	-3.41E-01	1	Unchanged Low
Q9NZP9	E17ef2	immediate early response 5	105.1683	157	146.761	136.3041	4.81E-01	5.76E-01	1	Unchanged Low
Q9UJA3	I12ef2	neutral sphingomyelinase	165.6408	147	146.8134	153.0756	-1.74E-01	-1.74E-01	1	Unchanged Low
Q99734	M12ef5	Notch homolog 2 (Drosophila)	220.4251	263	147.0111	210.2011	-5.84E-01	2.56E-01	1	Unchanged Low
O00411	C19cd1	polymerase (RNA) mitochondrial	120.5078	105	147.0481	124.1084	2.87E-01	-2.02E-01	1	Unchanged Low
P28347	P04gh1	TEA domain family member 1 (S <sup>t</sup> )	230.2101	174	147.0913	163.776	-6.46E-01	-4.04E-01	1	Unchanged Low
Q13819	G19gh1	cullin 4A	153.1592	218	147.2043	172.6621	-5.72E-02	5.07E-01	1	Unchanged Low
Q94929	O06ef8	KIAA0843 protein	108.7621	99.4	147.2921	118.4779	4.37E-01	-1.31E-01	1	Unchanged Low
Q9P026	A02ef8	HSPC134 protein	115.4895	184	147.3205	149.0331	3.51E-01	6.74E-01	1	Unchanged Low
P28067	D08ab5	major histocompatibility complex	128.7098	100	147.3934	125.4983	1.96E-01	5.85E-01	1	Unchanged Low
Q14126	E11ef7	desmoglein 2	426.8387	366	147.4196	313.3393	-1.53E+00	-2.23E-01	1	Unchanged Low
Q14267	P01cd1	regulatory factor X; 4 (Influences	127.7912	98.9	147.4351	124.7021	2.06E-01	-3.70E-01	1	Unchanged Low
P55197	H09ab2	myeloid/lymphoid or mixed-lineag	160.668	185	147.4439	146.3164	-1.24E-01	2.02E-01	1	Unchanged Low
Q9NP87	O20cd8	polymerase (DNA directed); mu	115.1765	66.7	147.4845	116.4497	3.57E-01	-4.10E-01	1	Unchanged Low
P04155	H0ef5	trefoil factor 1 (breast cancer; esl	258.058	136	147.487	180.4791	-8.07E-01	-9.25E-01	1	Unchanged Low
Q9C069	N02gh7	sec13-like protein	52.65015	424	147.5255	207.8565	1.49E+00	3.01E+00	1	Unchanged Low
P12270	G14cd2	translocated promoter region (to	104.4493	136	147.7447	129.4065	5.00E-01	3.81E-01	1	Unchanged Low
Q9uIG5	I14ef2	LPAP for lysophosphatidic acid r	218.3106	325	147.8779	230.2685	-5.62E-01	5.72E-01	1	Unchanged Low
O15453	P08cd5	NBR2	99.08545	108	147.9143	118.2765	5.78E-01	1.22E-01	1	Unchanged Low
Q9UNW8	F17cd8	G protein-coupled receptor	239.3255	347	148.021	244.7569	-6.93E-01	5.36E-01	1	Unchanged Low
P06746	H0ef5	polymerase (DNA directed); beta	142.5013	225	148.0351	171.8166	5.50E-02	6.58E-01	1	Unchanged Low
O15414	I08cd7	trinucleotide repeat containing 4	131.6219	199	148.0947	159.7305	1.70E-01	6.00E-01	1	Unchanged Low
O15259	L22ab7	nephronophthisis 1 (juvenile)	115.0436	110	148.3613	124.437	3.67E-01	-6.59E-02	1	Unchanged Low
Q9NR48	P05gh4	elF4E-transporter	106.343	178	148.4323	144.3142	4.81E-01	7.45E-01	1	Unchanged Low
Q9NP77	C10ef8	HSPC182 protein	171.17	175	148.5234	165.0639	-2.05E-01	3.60E-02	1	Unchanged Low
Q06587	P17cd1	ring finger protein 1	119.2377	127	148.6557	131.6381	3.18E-01	9.12E-02	1	Unchanged Low
Q9V5Z5	E22ef2	heme binding protein 1	181.0768	196	148.7681	175.2357	-2.84E-01	1.13E-01	1	Unchanged Low
O15327	I05cd4	Inositol polyphosphate-4-phosph	183.6815	131	148.785	154.5722	-3.04E-01	-4.85E-01	1	Unchanged Low
P49646	P19cd1	regulator of mitotic spindle assen	143.9463	91.9	148.8487	136.7074	4.83E-02	-2.95E-01	1	Unchanged Low
Q99809	F18cd5	conserved gene amplified in oste	134.0126	91.3	148.9901	124.7728	1.53E-01	-5.53E-01	1	Unchanged Low
Q9UBM1	G02cd7	phosphatidylethanolamine N-met	138.4849	122	149.0109	136.3565	1.06E-01	-1.88E-01	1	Unchanged Low
P16403	G04ab6	H1 histone family; member 2	427.1258	558	149.1016	377.9287	-1.52E+00	3.84E-01	1	Unchanged Low
O75503	B01ab4	ceroid-lipofuscinosis; neuronal 5	148.9991	75.4	149.1361	124.5021	1.33E-03	-9.83E-01	1	Unchanged Low
P15814	P20gh6	Immunoglobulin lambda-like polype	78.91644	144	149.2005	123.9169	9.19E-01	8.64E-01	1	Unchanged Low
Q03164	N01ab7	myeloid/lymphoid or mixed-lineag	157.0713	81.9	149.3538	129.4559	-7.26E-02	-9.39E-01	1	Unchanged Low
Q13624	B08ef6	Interleukin-1 enhancer binding fact	136.4076	130	149.4265	138.6386	1.32E-01	-6.85E-02	1	Unchanged Low
Q14118	M02ab5	dystroglycan 1 (dystrophin-assoc	105.7987	99	149.6192	118.1383	5.00E-01	-9.59E-02	1	Unchanged Low
Q13286	E20ab3	ceroid-lipofuscinosis; neuronal 3	240.521	302	149.6542	230.6187	-6.85E-01	3.27E-01	1	Unchanged Low
Q9v5Q0	E15gh7	fatty acid desaturase 3	117.0825	115	149.704	127.2281	3.55E-01	-2.72E-02	1	Unchanged Low
Q9P0R1	K08ef2	forkhead box P1	99.17408	114	149.7517	120.8481	5.95E-01	1.98E-01	1	Unchanged Low
P41182	C24ab5	C-cell CLU/lymphoma 6 (zinc fing	115.9704	85.9	149.8553	117.2275	3.70E-01	-4.34E-01	1	Unchanged Low
Q75497	K14cd6	microspherule protein 1	145.7927	163	149.9313	153.0143	4.04E-02	1.64E-01	1	Unchanged Low
Q14185	M19ab4	dedicator of cyto-kinesis 1	95.3322	112	150.0398	118.9819	6.54E-01	2.27E-01	1	Unchanged Low
Q95163	P05cd3	Inhibitor of kappa light polypeptid	203.0161	120	150.0489	157.6357	-4.35E-01	-7.60E-01	1	Unchanged Low
Q14508	L05ef7	WAP four-disulfide core domain	102.6084	201	150.0782	151.3745	5.49E-01	9.73E-01	1	Unchanged Low
P25942	M21ef7	tumor necrosis factor receptor su	110.0933	239	150.0883	166.2403	4.47E-01	1.12E+00	1	Unchanged Low
Q9V6E9	F15cd3	serine/threonine kinase 24 (STE	206.7079	225	150.1279	194.1145	-4.60E-01	1.25E-01	1	Unchanged Low
Q9UQF2	J21cd5	mitogen-activated protein kinase	229.9384	182	150.2902	187.4786	-6.13E-01	-3.38E-01	1	Unchanged Low
Q9Y285	D11ab5	phenylalanine-tRNA synthetase	179.7613	145	150.3716	158.2291	-2.58E-01	-3.14E-01	1	Unchanged Low
Q04762	F09ab4	cell matrix adhesion regulator	134.1594	176	150.3997	153.4581	1.65E-01	3.90E-01	1	Unchanged Low
Q9Y6J9	P19ef6	TAF5-like RNA polymerase II; p	77.59128	158	150.4181	128.6968	9.55E-01	1.03E+00	1	Unchanged Low
Q43913	C05ab8	origin recognition complex; subu	147.9187	168	150.4866	155.6272	2.48E-02	1.88E-01	1	Unchanged Low
P25208	M05cd1	nuclear transcription factor Y; be	106.4862	138	150.5231	131.7807	4.99E-01	3.77E-01	1	Unchanged Low
Q9H9X4	P03gh3	hypothetical protein FLJ1618	169.58	179	150.5879	173.1977	-3.32E-01	-7.94E-02	1	Unchanged Low
Q95287	P17cd4	myelin protein zero-like 1	127.461	121	150.7509	133.0095	2.42E-01	-7.72E-02	1	Unchanged Low
Q9UPG8	O05ab8	pleiomorphic adenoma gene-like	134.8747	165	150.9533	150.4388	1.62E-01	2.95E-01	1	Unchanged Low
P16333	H16ef5	NCK adaptor protein 1	237.1463	351	150.9549	246.4108	-6.52E-01	5.66E-01	1	Unchanged Low
Q14108	I22ab5	CD36 antigen (collagen type I re	155.2026	139	150.9785	148.3416	-3.98E-02	-1.61E-01	1	Unchanged Low
Q9UF9	O05cd5	CCR4-NOT transcription comple	162.9025	208	151.0687	174.1041	-1.09E-01	3.55E-01	1	Unchanged Low
O15242	O19ab8	nandilysn (N-arginine dibasic cor	210.0164	198	151.1245	188.2788	-4.75E-01	-8.72E-02	1	Unchanged Low
Q13442	N15ef3	PDGF $\alpha$ associated protein 1	156.1376	188	151.1314	165.0545	-4.70E-02	2.67E-01	1	Unchanged Low
Q97755	A15ef6	phosphatidylinositol 4-phosphate	112.2177	146	151.3432	138.4804	4.32E-01	3.78E-01	1	Unchanged Low
Q9NZV1	E09gh2	cysteine-rich motor neuron 1	112.5932	99.1	151.3541	121.0073	4.27E-01	-1.85E-01	1	Unchanged Low
Q95195	C09ab7	MAX dimerization protein	136.8998	254	151.5662	180.6838	1.47E-01	8.89E-01	1	Unchanged Low
Q95671	J14ab2	acetylserotonin O-Methyltransfer	99.67178	98.5	151.7064	116.6189	6.05E-01	-1.74E-02	1	Unchanged Low
Q9Y658	A09ef2	RNA helicase	112.9715	95.3	151.8988	120.0494	4.27E-01	-2.46E-01	1	Unchanged Low
Q9BTU6	N12gh6	phosphatidylinositol 4-kinase typ	97.30862	178	151.965	142.5367	6.43E-01	8.74E-01	1	Unchanged Low
Q9UPN6	G04ef8	KIAA1116 protein	127.681	113	152.0268	130.9048	2.52E-01	-1.76E-01	1	Unchanged Low
Q90170	J03ab2	aryl hydrocarbon receptor intera	555.1127	223	152.0508	310.1793	-1.87E+00	-1.31E+00	1	Unchanged Low
Q9UJW6	P01ef3	activity-regulated cytoskeleton-a	221.8559	185	152.1474	186.4423	-5.44E-01	-2.60E-01	1	Unchanged Low
Q9HCT0	N02ef8	fibroblast growth factor 22	157.7471	126	152.2042	145.1536	-5.16E-02	-3.30E-01	1	Unchanged Low
Q15459	O03cd6	splicing factor 3a; subunit 1; 120l	163.4432	145	152.3945	153.5048	-1.01E-01	-1.76E-01	1	Unchanged Low
Q95400	G18cd6	CD2 antigen (cytoplasmic tail) bl	192.2313	238	152.5257	194.1745	-3.34E-01	3.07E-01	1	Unchanged Low
P07854	M05ab3	fumarate hydratase	121.2546	142	152.5652	138.7259	3.31E-01	2.31E-01	1	Unchanged Low
Q9H6Z5	C16gh5	hypothetical protein FLJ21634	101.1467	152	152.6745	135.2933	5.94E-01	5.88E-01	1	Unchanged Low
Q9HCN8	A05gh1	stromal cell-derived factor 2-like	136.5604	128	152.9097	139.1775	1.63E-01	-9.27E-02	1	Unchanged Low
Q92890	A24cd4	ubiquitin fusion degradation 1-lik	157.2559	220	152.9538	176.6159	-4.00E-02	4.82E-01	1	Unchanged Low

O43324	N24cd4	eukaryotic translation elongation	150.6748	112	152.9613	138.6164	2.17E-02	-4.25E-01	1	Unchanged Low
Q9NVU8	H10gh2	hypothetical protein FLJ10496	145.4398	119	152.9651	139.1241	7.28E-02	-2.90E-01	1	Unchanged Low
Q9NQW6	H01ef4	anillin; actin binding protein (scr)	113.8655	85.6	152.992	117.4953	4.26E-01	-4.11E-01	1	Unchanged Low
Q9NWY4	L01gh2	mitochondrial ribosomal protein l	173.4347	107	153.0783	144.3461	-1.80E-01	-7.03E-01	1	Unchanged Low
Q9UBV8	M13cd8	PEF protein with a long N-termin	148.0371	144	153.0828	148.3188	4.84E-02	-4.15E-02	1	Unchanged Low
P15328	F10ab3	folate receptor 1 (adult)	152.5051	123	153.1163	142.7655	5.77E-03	-3.14E-01	1	Unchanged Low
Q9Y5B3	B01cd6	NS1-associated protein 1	143.6263	177	153.2797	157.8847	9.38E-02	2.99E-01	1	Unchanged Low
Q07326	M08ab8	phosphatidylinositol glycan; clas	132.6521	93	153.3084	126.3257	2.09E-01	-5.12E-01	1	Unchanged Low
Q75396	M12cd5	SEC22 vesicle trafficking protein	143.9018	153	153.3626	150.1024	9.19E-02	8.88E-02	1	Unchanged Low
Q9Y228	D09ef2	CG1-09 protein	117.2943	110	153.5282	126.8764	3.88E-01	-9.52E-02	1	Unchanged Low
Q9H3P7	N05gh5	golgi phosphoprotein 1	251.3681	258	153.65	220.9899	-7.10E-01	3.73E-02	1	Unchanged Low
O56578	E03cd5	cysteine/arginine-rich protein	339.3692	195	153.797	229.3684	-1.14E+00	-8.00E-01	1	Unchanged Low
P17026	M04cd4	zinc finger protein 22 (KOX 15)	152.7226	68.3	153.8793	131.6407	1.08E-02	-7.90E-01	1	Unchanged Low
Q9Y3N9	M05gh7	olfactory receptor; family 2; subf	127.2527	137	153.9228	139.4653	2.75E-01	-1.09E-01	1	Unchanged Low
Q9BYT8	K08gh7	neurolysin (metalloprotease M3	85.89781	193	154.0005	144.2719	8.41E-01	1.16E+00	1	Unchanged Low
Q9UHQ7	F02ef7	pp21 homolog	119.2248	136	154.0057	136.5651	3.69E-01	1.95E-01	1	Unchanged Low
O50921	A22ab7	HUS1 checkpoint homolog (S. po	148.5718	204	154.125	169.0172	5.28E-02	4.60E-01	1	Unchanged Low
O00400	D05ab2	acetyl-Coenzyme A transporter	196.9505	124	154.2012	158.3654	-3.53E-01	-6.68E-01	1	Unchanged Low
Q9Y690	H01gh6	mortality factor 4	253.2426	259	154.2307	222.1522	-7.15E-01	3.23E-02	1	Unchanged Low
Q9NZL9	L24ef7	methionine adenosyltransferase	128.4144	99.7	154.2681	127.4733	2.65E-01	-3.65E-01	1	Unchanged Low
O60563	A05ab4	cyclin T1	179.5706	171	154.2911	168.3854	-2.19E-01	-6.81E-02	1	Unchanged Low
P20591	M03ab7	mycovirus (Influenza virus) rest	459.0611	873	154.338	495.4752	-1.57E+00	9.27E-01	1	Unchanged Low
Q9BQC6	P14gh5	mitochondrial ribosomal protein t	188.6422	74.3	154.357	139.1028	-2.89E-01	-1.34E+00	1	Unchanged Low
P28838	J02ef1	leucine aminopeptidase 3	409.1007	383	154.3828	315.6553	-1.41E+00	-9.33E-02	1	Unchanged Low
Q9NZES	P08ef1	hypothetical protein LOC51319	135.1502	171	154.3904	153.3881	1.92E-01	3.36E-01	1	Unchanged Low
Q9NX47	K10gh2	hypothetical protein FLJ20445	299.3918	338	154.4327	263.9291	-5.95E-01	1.75E-01	1	Unchanged Low
O60612	K11cd2	supervillin	113.6228	270	154.4497	179.421	4.43E-01	1.25E+00	1	Unchanged Low
O00559	F22cd4	estrogen receptor binding site as	181.5726	147	154.679	160.9495	-2.31E-01	-3.09E-01	1	Unchanged Low
Q9NUU9	E17gh3	hypothetical protein F23149_1	140.3785	224	154.7106	172.9723	1.40E-01	6.73E-01	1	Unchanged Low
P22059	C10ab8	oxysterol binding protein	133.2924	93.6	154.8714	127.2507	-5.10E-01	1.80E-01	1	Unchanged Low
O00408	I05ef5	phosphodiesterase 2A; cGMP-sli	860.2983	159	154.9588	394.9107	-2.47E+00	-2.34E+00	1	Unchanged Low
Q94935	P22ef7	SAC1 suppressor of aden1 multia	146.0417	128	154.9914	142.9113	8.58E-02	-1.94E-01	1	Unchanged Low
P41134	H15ef5	inhibitor of DNA binding 1; domr	434.1844	292	155.0439	293.8674	-1.49E+00	-5.70E-01	1	Unchanged Low
P24407	M08ab7	mel transforming oncogene (der	224.1153	189	155.1664	189.5599	-5.30E-01	-2.43E-01	1	Unchanged Low
O00232	N05ab8	proteasome (prosome); macropak	122.517	139	155.2465	139.0276	3.42E-01	1.85E-01	1	Unchanged Low
Q01432	G04ab2	adenosine monophosphate deacti	111.1766	117	155.341	127.7664	4.83E-01	7.10E-02	1	Unchanged Low
Q13525	G15cd4	interleukin 1 receptor-like 2	136.0802	130	155.4674	140.5051	1.92E-01	-6.63E-02	1	Unchanged Low
Q16611	N04ab3	BCL2-antagonist/killer 1	280.4131	194	155.5414	210.0516	-8.50E-01	-5.30E-01	1	Unchanged Low
Q9NP43	C11gh5	hypothetical protein STRAIT114q	112.5378	85.5	155.5531	117.8671	4.67E-01	-3.96E-01	1	Unchanged Low
P42702	D14gh7	LIS1-interacting protein NUDEL;	137.8235	131	155.5611	141.4354	1.75E-01	-7.41E-02	1	Unchanged Low
Q05940	P07ef5	solute carrier family 18 (vesicular	374.4901	112	155.6189	120.0363	7.51E-01	2.77E-01	1	Unchanged Low
Q9Y3Q5	H18cd6	putative DNA/chromatin binding I	75.96908	153	155.637	227.6447	-1.27E+00	-1.29E+00	1	Unchanged Low
Q15756	I08ab7	potassium inwardly-rectifying ch	149.0689	150	155.6726	127.0621	1.04E+00	9.77E-01	1	Unchanged Low
O75386	M17cd3	tubby like protein 3	128.6914	80.9	155.7504	128.583	6.33E-02	-8.81E-01	1	Unchanged Low
P50750	D03ef5	cydin-dependent kinase 9 (CDC	270.8229	82.7	155.7811	122.3782	2.76E-01	-6.39E-01	1	Unchanged Low
Q9NWY6	A18gh3	hypothetical protein FLJ20531	91.85185	215	155.8317	213.7777	-7.97E-01	-3.35E-01	1	Unchanged Low
P50391	K05cd1	pancreatic polypeptide receptor *	136.5278	130	156.1332	125.9903	7.65E-01	5.01E-01	1	Unchanged Low
Q9NQX7	L20gh6	tRNA selenocysteine associated	258.434	112	156.1953	134.9143	1.94E-01	-2.85E-01	1	Unchanged Low
O75354	A15ab4	ectonucleoside triphosphate dip	366.4989	287	156.2449	233.9363	-7.26E-01	1.52E-01	1	Unchanged Low
Q9H832	L12gh5	hypothetical protein FLJ13855	173.4437	258	156.4638	267.133	-1.30E+00	-5.81E-01	1	Unchanged Low
Q9UBW8	F18ef1	COP9 constitutive morphomorph	102.8052	307	156.9292	212.3427	-1.44E+01	8.22E-01	1	Unchanged Low
P14136	E23ab5	glia fibrillary acidic protein	108.166	111	157.0119	123.4686	6.11E-01	1.05E-01	1	Unchanged Low
Q9NYF3	F08ef1	chromosome 5 open reading frar	121.4116	86.6	157.2761	117.3353	5.40E-01	-3.21E-01	1	Unchanged Low
Q15056	A09gh2	Williams-Beuren syndrome chro	202.4969	94.3	157.5806	124.4392	3.76E-01	-3.64E-01	1	Unchanged Low
O15534	I16ab8	period homolog 1 ( <i>Drosophila</i> )	237.2007	124	157.6763	161.3602	-3.61E-01	-7.09E-01	1	Unchanged Low
Q9Y399	O21ef2	mitochondrial ribosomal protein t	229.9134	143	157.7195	179.3665	-5.89E-01	-7.28E-01	1	Unchanged Low
O14972	A04cd6	Down syndrome critical region g	230.0837	139	157.7339	175.5893	-5.44E-01	-7.25E-01	1	Unchanged Low
Q14113	M15ab2	AE binding protein 1	124.9796	267	157.7386	218.3678	-5.45E-01	2.16E-01	1	Unchanged Low
O25755	O18cd5	RAB36; member RAS oncogene	132.9919	95.3	157.955	126.0667	3.38E-01	-3.92E-01	1	Unchanged Low
Q9NP43	D13cd5	enhancer of Invasion 10	104.2128	97	158.0474	129.3518	2.49E-01	-4.55E-01	1	Unchanged Low
Q9Y6E9	N24cd7	sirn1 silent mating type Informal	111.8557	121	158.1023	127.8011	6.01E-01	2.17E-01	1	Unchanged Low
Q9Y5B8	D17cd8	NME7	92.69165	143	158.1227	140.9006	5.00E-01	4.48E-01	1	Unchanged Low
P49642	I21ab8	primase; polypeptide 1 (49kD)	135.2376	116	158.2444	122.4719	7.72E-01	3.30E-01	1	Unchanged Low
O60660	J04ab2	ash2 (absent; small; or homeotic	274.3502	267	158.2887	121.2327	2.27E-01	-9.47E-01	1	Unchanged Low
Q9H251	O08gh7	cadherin related 23	113.1038	177	158.3372	203.1619	-7.93E-01	-6.34E-01	1	Unchanged Low
Q9Y6C2	A22cd7	elastin microfibril interface locate	107.9751	184	158.4524	151.9031	4.86E-01	7.03E-01	1	Unchanged Low
O95825	D13cd5	crystallin; zeta (quinone reducta	144.0183	92.2	158.6648	119.6097	5.55E-01	-2.28E-01	1	Unchanged Low
Q9JHG3	J02ef2	premycysteine lyase	250.3969	133	158.6719	145.1487	1.40E-01	-1.17E-01	1	Unchanged Low
O00629	J18ab6	karyopherin alpha 4 (importin alp	518.8184	207	158.8419	205.2993	-6.57E-01	-2.77E-01	1	Unchanged Low
Q15397	B14gh1	KIAA0020 gene product	109.8533	295	158.8458	324.141	-1.71E-01	-8.16E-01	1	Unchanged Low
Q14999	H01gh1	KIAA0076 gene product	71.35119	134	158.9595	134.3527	5.33E-01	2.89E-01	1	Unchanged Low
Q12772	M18cd2	sterol regulatory element binding	158.6108	173	159.0037	134.6153	1.16E+00	1.28E+00	1	Unchanged Low
O75150	F09gh1	ring finger protein 40	129.2351	94.6	159.1986	137.4667	5.34E-03	-7.46E-01	1	Unchanged Low
O43423	L07gh6	addc1 (leucine-rich) nuclear pho	140.3006	149	159.2321	152.3442	3.01E-01	3.84E-01	1	Unchanged Low
O43311	D12cd8	muscleblind-like ( <i>Drosophila</i> )	165.2243	143	159.4372	147.5392	1.84E-01	2.63E-02	1	Unchanged Low
Q9NYX4	B07ef4	calcyon; D1 dopamine receptor-ii	207.2791	147	159.5302	171.42	-3.78E-01	-4.91E-01	1	Unchanged Low
Q9HD71	G04gh4	hypothetical nuclear factor SBB1	123.7874	140	159.5491	141.2517	3.66E-01	1.82E-01	1	Unchanged Low
Q9NZH2	N03cd8	replication initiation region protei	225.0949	179	159.6113	187.9443	-4.96E-01	-3.30E-01	1	Unchanged Low
Q9NVH1	B05gh3	hypothetical protein FLJ10737	137.4673	217	159.6304	171.2625	2.16E-01	6.57E-01	1	Unchanged Low
Q9NVG3	B11gh3	hypothetical protein FLJ10751	96.28296	105	159.6829	120.1783	7.30E-01	1.19E-01	1	Unchanged Low
P52179	A21cd4	myomesin 1 (skelein) (185kD)	157.0608	94	159.8272	136.9676	2.52E-02	-7.40E-01	1	Unchanged Low
O94815	B08cd3	frizzled homolog 1 ( <i>Drosophila</i> )	93.97877	101	159.9198	118.2939	7.67E-01	1.04E-01	1	Unchanged Low
Q9UYB9	G01ef4	heat shock 27kD protein family; r	98.97552	102	160.1725	120.3216	6.94E-01	4.08E-02	1	Unchanged Low
Q9NVX7	G18gh3	hypothetical protein FLJ10450	111.51956	121	160.2507	130.905	5.23E-01	1.17E-01	1	Unchanged Low
O95704	A02cd6	FE65-like protein 2	99.35088	115	160.3239	124.7475	6.90E-01	2.06E-01	1	Unchanged Low

P19801	A23ab2	amilioride binding protein 1 (amin	164.6296	68.3	160.3477	131.0836	-3.80E-02	-1.27E+00	1	Unchanged Low
Q43709	L18ef3	Williams Beuren syndrome chrm	127.8538	134	160.4415	140.7665	3.28E-01	6.84E-02	1	Unchanged Low
Q12839	N24ef1	H326	109.677	116	160.6141	128.6095	5.50E-01	8.26E-02	1	Unchanged Low
Q43503	D10ab8	RAD51 homolog C ( <i>S. cerevisiae</i> )	96.34779	97.6	160.6551	118.1934	7.38E-01	1.83E-02	1	Unchanged Low
Q76988	J10cd4	CD163 antigen	87.73563	177	160.8614	141.7231	8.75E-01	1.01E-00	1	Unchanged Low
Q96015	F22cd5	dyneln; axonemal; light polypepti	94.54055	251	160.9963	168.8465	7.68E-01	1.41E-00	1	Unchanged Low
Q92524	L11ab8	proteasome (prosome; macropai	398.6515	220	161.0391	259.1219	-1.30E+00	-8.52E-01	1	Unchanged Low
Q92692	B06ab8	poliovirus receptor-related 2 (her	302.7185	317	161.2569	260.2905	-9.09E-01	6.60E-02	1	Unchanged Low
Q9Y6V8	H16cd7	Sec23-interacting protein p125	104.2429	131	161.2684	132.2965	6.30E-01	3.34E-01	1	Unchanged Low
Q9NZ78	J16gh3	uncharacterized bone marrow pr	107.2001	127	161.3587	131.7449	5.90E-01	2.41E-01	1	Unchanged Low
Q15120	G15cd1	pyruvate dehydrogenase kinase;	96.64061	107	161.6468	121.6758	7.42E-01	1.43E-01	1	Unchanged Low
P35241	F22ab8	radixin	276.6012	213	161.7003	216.9693	-7.74E-01	-3.80E-01	1	Unchanged Low
Q9Y326	D23zf2	brain specific protein	359.3582	160	161.7123	227.0406	-1.15E+00	-1.17E+00	1	Unchanged Low
Q92600	J03cd5	RCD1 required for cell differentia	115.6633	145	161.7142	140.923	4.84E-01	3.30E-01	1	Unchanged Low
Q00487	N14cd5	26S proteasome-associated pad-	329.3518	275	161.8834	255.4035	-1.02E+00	-2.60E-01	1	Unchanged Low
Q9Y689	P21cd7	ADP-ribosylation factor-like 5	137.7737	159	161.8965	152.9708	2.33E-01	2.09E-01	1	Unchanged Low
Q9UL88	P05cd8	CMP-NeuAC:(beta)-N-acetylgal	91.01128	121	161.9148	124.5785	8.31E-01	4.09E-01	1	Unchanged Low
Q60897	L09cd7	RAB; member of RAS oncogene	89.32474	112	162.0127	120.9939	8.59E-01	3.22E-01	1	Unchanged Low
P51809	J05cd2	synaptobrevin-like 1	228.3546	141	162.1052	177.2043	-4.94E-01	-6.94E-01	1	Unchanged Low
Q75581	A03ab7	low density lipoprotein receptor-	122.4708	125	162.1159	136.4067	4.05E-01	2.53E-02	1	Unchanged Low
Q43795	F12ef4	myosin class I; myh-1c	259.4543	282	162.1237	234.504	-6.78E-01	1.20E-01	1	Unchanged Low
Q14188	H17ef5	transcription factor Dp-2 (E2F dlr	107.308	204	162.1489	157.7494	5.96E-01	9.25E-01	1	Unchanged Low
P06280	B07ab3	galactosidase; alpha	178.0238	304	162.2871	214.6169	-1.34E-01	7.70E-01	1	Unchanged Low
Q14541	I17ab7	hepatocyte nuclear factor 4; gam	549.897	283	162.4659	331.895	-1.76E-00	-9.57E-01	1	Unchanged Low
P57723	E17gh8	poly(R) binding protein 4	186.2845	231	162.5267	193.1283	-1.97E-01	3.08E-01	1	Unchanged Low
Q9NWU3	A24gh3	DEAD/H (Asp-Glu-Ala-Asp/His) t	154.71	104	162.6529	140.5056	7.22E-02	-5.71E-01	1	Unchanged Low
Q9NPs5	J16ef6	nudix (nucleoside diphosphate) II	107.1863	98.4	162.6592	122.7442	6.02E-01	-1.24E-01	1	Unchanged Low
Q9Y3C5	B19ef3	ring finger protein 11	160.0631	164	162.7518	162.3366	2.40E-02	3.68E-02	1	Unchanged Low
Q9NWX3	B01gh2	chromosome 20 open reading fra	98.58482	95.6	162.7744	118.9844	7.23E-01	-4.44E-02	1	Unchanged Low
P52742	I22cd3	zinc finger protein 135 (clone pH	61.4141	121	162.8382	121.6363	1.00E+00	5.68E-01	1	Unchanged Low
Q9Y313	D17ef2	PTD013 protein	90.25232	118	163.4053	123.3545	8.56E-01	3.67E-01	1	Unchanged Low
Q9P2W9	B11ef4	synatxin 18	128.6426	188	163.4277	160.0555	3.45E-01	5.48E-01	1	Unchanged Low
P14778	F09ab6	Interleukin 1 receptor; type I	264.5401	539	163.4432	322.4754	-6.95E-01	1.03E+00	1	Unchanged Low
Q15464	H12ef5	SHB (Src homology 2 domain co	284.291	301	163.5373	249.6096	-7.98E-01	8.24E-02	1	Unchanged Low
O15444	H07cd2	small inducible cytokine subfamily	244.6426	97.1	163.6053	168.4558	-5.80E-01	-1.33E+00	1	Unchanged Low
P49796	P14ef4	regulator of G-protein signalling :	220.2769	99.3	163.6222	161.0774	-4.29E-01	-1.15E+00	1	Unchanged Low
Q9NU57	B04gh3	hypothetical protein FLJ1164	81.76063	114	163.6422	119.7258	1.00E+00	4.77E-01	1	Unchanged Low
P48651	L11ef3	phosphatidylserine synthase 1	211.8695	139	163.6792	171.5708	-3.72E-01	-6.06E-01	1	Unchanged Low
Q07706	F15cd4	tetracycline transporter-like prote	143.0791	144	163.7206	150.2019	1.94E-01	7.31E-03	1	Unchanged Low
O75143	I12ef5	KIAA0652 gene product	106.5331	155	163.7697	141.6405	6.20E-01	5.37E-01	1	Unchanged Low
O75039	L19gh1	KIAA0451 gene product	174.142	135	163.8572	157.7714	-8.78E-02	-3.64E-01	1	Unchanged Low
P02261	M10gh6	H2A histone family; member N	93.48591	273	163.8621	176.9259	8.10E-01	1.55E+00	1	Unchanged Low
Q9H9A0	L20gh5	hypothetical protein FLJ12895	86.42599	139	163.8655	126.7707	9.27E-01	5.84E-01	1	Unchanged Low
Q9NV35	J21gh3	hypothetical protein FLJ10956	99.15342	154	164.4852	139.1489	7.30E-01	6.33E-01	1	Unchanged Low
Q9P1G8	C05gh4	WW domain-containing adapter	119.4436	182	164.5311	155.3256	4.62E-01	6.08E-01	1	Unchanged Low
P26368	D11cd7	U2 small nuclear ribonucoprotein	217.0564	107	164.8861	163.126	-3.97E-01	-1.01E+00	1	Unchanged Low
Q9BSZ7	E11gh8	DEAD/H (Asp-Glu-Ala-Asp/His) t	130.7858	111	164.9084	135.6059	3.34E-01	-2.35E-01	1	Unchanged Low
Q9Y391	G23ef2	androgen-regulated short-chain c	222.3497	128	164.9823	171.7067	-4.31E-01	-7.99E-01	1	Unchanged Low
Q9NYR5	E05ef3	HSPC126 protein	99.37243	110	165.2098	124.8579	7.33E-01	1.46E-01	1	Unchanged Low
P05165	N12ab7	propionyl Coenzyme A carboxyla	100.892	120	165.6902	128.9755	7.16E-01	2.54E-01	1	Unchanged Low
Q9NPf4	O21gh3	O-sialylglycoprotein endopeptidase	103.8223	112	165.9718	127.3658	6.77E-01	1.13E-01	1	Unchanged Low
P16106	D01cd3	H3 histone family; member K	99.19006	130	166.1216	131.6683	7.44E-01	3.67E-01	1	Unchanged Low
P35249	O03ef5	replication factor C (activator 1)	105.2406	98.7	166.2092	123.3812	6.59E-01	-9.27E-02	1	Unchanged Low
P28702	P18gh1	retinoid X receptor; beta	74.914	142	166.2214	127.7277	1.15E+00	9.23E-01	1	Unchanged Low
P49574	K14ab4	casein kinase 1; epsilon	99.33956	145	166.3564	136.8564	7.44E-01	5.44E-01	1	Unchanged Low
Q9NW2	I03gh2	DnaJ (Hsp40) homolog; subfamily	247.7907	235	166.4412	126.5041	-5.74E-01	-7.47E-02	1	Unchanged Low
O14672	I01ab2	a disintegrin and metalloprotein	378.0042	226	166.5417	256.8185	-1.18E+00	-7.43E-01	1	Unchanged Low
Q9Y5B9	I20cd7	chromatin-specific transcription	163.0543	188	166.6045	174.4726	3.11E-02	2.04E-01	1	Unchanged Low
Q9H9J2	H22gh5	mitochondrial ribosomal protein l	206.4248	256	166.8142	209.7386	-3.07E-01	3.10E-01	1	Unchanged Low
P23759	G06ab8	paired box gene 7	92.41833	200	166.8514	153.0178	8.52E-01	1.11E+00	1	Unchanged Low
Q16643	L05ab4	drebrin 1	265.008	152	166.9734	194.7352	-6.66E-01	-8.00E-01	1	Unchanged Low
P48454	I21cd1	protein phosphatase 3 (formerly :	105.9496	169	167.0428	147.2674	6.57E-01	6.72E-01	1	Unchanged Low
Q9Y508	F21ef1	zinc finger protein 313	331.595	395	167.2366	297.9139	-9.88E-01	2.52E-01	1	Unchanged Low
P19474	G09cd2	Sjogren syndrome antigen A1 (S:	301.1776	183	167.414	217.1349	-8.47E-01	-7.20E-01	1	Unchanged Low
P46109	N13ab5	v-crk sarcoma virus CT10 oncogene	151.2065	141	167.7716	153.202	1.50E-01	-1.05E-01	1	Unchanged Low
P54855	B19cd4	UDP glycosyltransferase 2 family	137.8939	127	168.8346	144.2152	2.83E-01	-1.20E-01	1	Unchanged Low
Q14242	H14cd1	selecln P ligand	112.9679	130	169.1914	136.8261	5.72E-01	1.98E-01	1	Unchanged Low
Q9BS51	P17gh8	hypothetical protein FLJ14525	86.75908	113	167.974	122.482	9.53E-01	3.76E-01	1	Unchanged Low
Q9Y382	L23ef1	homolog of yeast exosomal core	152.0751	140	167.9915	153.2264	1.44E-01	-1.23E-01	1	Unchanged Low
P31391	N03cd1	somatostatin receptor 4	147.3942	92.5	168.0254	135.9754	1.89E-01	-6.72E-01	1	Unchanged Low
O60623	O03ab4	diphtheria toxin resistance protein	210.9658	170	168.0762	183.009	-3.28E-01	-3.12E-01	1	Unchanged Low
Q99595	L24ab8	plakophilin 2	362.9423	211	168.1655	247.4823	-1.11E+00	-7.80E-01	1	Unchanged Low
B21gh7	leukocyte immunoglobulin-like re	139.2571	234	168.1829	180.4867	2.72E-01	7.49E-01	1	Unchanged Low	
Q01658	P18ab5	down-regulator of transcription 1:	205.2249	122	168.2606	165.0596	-2.87E-01	-7.54E-01	1	Unchanged Low
Q9HCS4	P10gh7	HMG-box transcription factor TCI	76.48423	156	168.2926	133.5936	1.14E+00	1.03E+00	1	Unchanged Low
Q9P035	N20er2	butyrate-induced transcript 1	102.716	142	168.3034	137.5999	7.12E-01	4.65E-01	1	Unchanged Low
Q9C0K7	P24gh3	amyotrophic lateral sclerosis 2 (t)	102.352	108	168.4355	126.1345	7.19E-01	7.24E-02	1	Unchanged Low
Q9NYF4	I13ef3	chromosome 5 open reading frer	89.72908	137	168.4424	131.7509	9.09E-01	6.11E-01	1	Unchanged Low
P30042	M19cd4	chromosome 21 open reading frer	98.84241	97.5	168.5171	121.6076	7.70E-01	-2.03E-02	1	Unchanged Low
Q75325	K16cd6	glioma amplified on chromosome	116.3239	83.3	168.5172	122.705	5.35E-01	-4.62E-01	1	Unchanged Low
Q9Y670	N01ef2	transient receptor potential cation	96.41626	90.8	168.5297	118.5764	8.06E-01	-8.69E-02	1	Unchanged Low
Q9UPR8	I14ef8	KIAA1084 protein	101.3235	111	168.5336	126.797	7.34E-01	1.26E-01	1	Unchanged Low
Q9Y2X7	I21ef4	G protein-coupled receptor kinas	160.7403	167	168.7352	165.5706	7.00E-02	5.72E-02	1	Unchanged Low
P47872	D24cd1	secretin receptor	174.6672	209	168.738	184.1802	-4.98E-02	2.60E-01	1	Unchanged Low
O43535	C17cd4	receptor-interacting serine-threon	272.5279	388	168.7722	276.5664	-6.91E-01	5.11E-01	1	Unchanged Low
P32321	P14ab5	dCMP deaminase	218.5685	60.1	168.8404	149.1554	-3.72E-01	-1.86E-01	1	Unchanged Low

Q43612	J16ab4	hypocrellin (orexin) neuropeptide	66.45691	194	168.9064	143.2577	1.35E+00	1.55E+00	1	Unchanged Low
Q92874	M15ab4	deoxyribonuclease H-like 2	218.1787	146	168.9596	177.8201	-3.69E-01	-5.76E-01	1	Unchanged Low
Q9UI90	I15ef8	PRO0038 protein	89.17218	389	168.9849	215.51	9.22E-01	2.12E+00	1	Unchanged Low
P30519	N05ab6	heme oxygenase (decycling) 2	566.3897	387	169.1269	380.9032	-1.79E+00	-5.99E-01	1	Unchanged Low
Q9NVE7	D03gh3	hypothetical protein FLJ10782	141.6695	148	169.2644	152.9293	2.57E-01	6.16E-02	1	Unchanged Low
Q9P010	A14ef8	HSPC154 protein	227.9143	246	169.4393	214.317	-4.28E-01	1.08E-01	1	Unchanged Low
Q9UH59	M04cd8	bromodomain-containing 7	147.6635	103	169.5045	139.9456	1.99E-01	-5.24E-01	1	Unchanged Low
Q9UM82	E01cd6	spermatogenesis associated 2	230.7114	221	169.6678	207.1298	-4.43E-01	-6.20E-02	1	Unchanged Low
Q9P2Y4	N14ef1	zinc finger protein 219	105.6753	175	169.7666	150.1216	6.84E-01	7.27E-01	1	Unchanged Low
Q9GZS3	H19gh7	recombination protein REC14	124.7245	162	169.9984	152.3724	4.47E-01	3.81E-01	1	Unchanged Low
P07686	J17ab3	hexosaminidase B (beta polypep	217.0423	135	170.0092	174.0094	-3.52E-01	-6.85E-01	1	Unchanged Low
Q9NZV6	L06ef2	selecnoprotein X; 1	241.3633	202	170.0232	204.3052	-5.05E-01	-2.60E-01	1	Unchanged Low
O14678	E17cd1	ATP-binding cassette; sub-family	77.65216	127	170.0525	124.9148	1.13E+00	7.10E-01	1	Unchanged Low
P29972	O04ab2	aquaporin 1 (channel-forming int	309.1218	134	170.2078	204.2885	-8.61E-01	-1.21E+00	1	Unchanged Low
O95373	D03cd6	RAN binding protein 7	247.4368	113	170.45	177.0459	-5.38E-01	-1.13E+00	1	Unchanged Low
Q15436	O12cd6	Sec23 homolog A (S. cerevisiae)	90.5071	100	170.9386	120.3545	9.25E-01	1.52E-01	1	Unchanged Low
Q9BQ67	K23gh8	glutamate rich WD repeat protein	140.3198	112	170.966	141.0924	2.85E-01	-3.25E-01	1	Unchanged Low
P35321	D21gh6	small proline-rich protein 1A	62.28271	237	171.0104	156.8515	1.46E+00	1.93E+00	1	Unchanged Low
Q9UPQ8	I10ef8	KIAA1094 protein	76.76245	123	171.0467	123.4833	1.16E+00	6.76E-01	1	Unchanged Low
O43292	A19cd4	GPA1P anchor attachment prot	95.36294	924	171.0704	119.6038	8.43E-01	-4.59E-02	1	Unchanged Low
Q9UBM3	G02cd1	proteasome (prosome; macropain	287.8026	204	171.1554	221.0285	-7.49E-01	-4.93E-01	1	Unchanged Low
P19338	M20ab7	nudotin	148.8642	87.6	171.2094	135.8947	2.02E-01	-7.65E-01	1	Unchanged Low
Q9NP53	E17gh1	sperm associated antigen 4	111.172	135	171.4356	139.3341	6.25E-01	2.84E-01	1	Unchanged Low
O00442	J12cd3	RTC domain containing 1	274.6701	279	171.531	241.6967	-6.79E-01	2.20E-02	1	Unchanged Low
P28356	D09ef1	homeobox D9	84.5638	108	171.5949	120.5873	1.02E+00	3.21E-01	1	Unchanged Low
P49447	G06ef1	cytchrome b-561	174.7152	167	171.6447	171.1671	-2.56E-02	-6.39E-02	1	Unchanged Low
Q9UQA4	P18cd4	nuclear factor (erythroid-derived	227.4253	470	171.8949	289.7702	-4.04E-01	1.05E+00	1	Unchanged Low
O15254	D09ab2	acyl-Coenzyme A oxidase 3; pris	192.2301	192	172.0218	185.2853	-1.60E-01	-4.71E-03	1	Unchanged Low
Q9NW66	B11gh2	hypothetical protein FLJ20559	198.7861	220	172.0261	197.0098	-2.09E-01	1.48E-01	1	Unchanged Low
Q75391	M08cd5	sperm associated antigen 7	154.1159	140	172.0658	155.2376	1.59E-01	-1.43E-01	1	Unchanged Low
Q92859	H19cd2	solute carrier family 21 (prostagl	86.25485	102	172.112	120.1434	9.97E-01	2.43E-01	1	Unchanged Low
O00499	G06ab2	bridging Integrator 1	162.8584	111	172.4453	148.8447	8.25E-02	-5.50E-01	1	Unchanged Low
Q14197	J05ab6	immature colon carcinoma transci	90.92583	102	172.5526	121.725	9.24E-01	1.62E-01	1	Unchanged Low
Q9NXS9	K15gh2	hypothetical protein FLJ20071	121.4575	103	172.5552	132.3749	5.07E-01	-2.36E-01	1	Unchanged Low
Q75954	N18cd6	tetraspan transmembrane 4 super	83.06795	119	172.5557	124.8565	1.05E+00	5.18E-01	1	Unchanged Low
Q9UJV9	E17cd8	lifeguard	75.6	172.6495	134.9529	1.41E-01	-1.05E+00	1	Unchanged Low	
P82912	F10gh5	mitochondrial ribosomal protein t	105.0578	196	172.7091	158.0886	7.17E-01	9.03E-01	1	Unchanged Low
Q12918	J02ab6	killer cell lectin-like receptor sub	205.6225	290	172.8141	222.8453	-2.51E-01	4.97E-01	1	Unchanged Low
Q14789	E01ab6	golgi autoantigen; golgi subfamily	96.09162	194	173.0059	154.2154	8.48E-01	1.01E+00	1	Unchanged Low
Q04206	I23ef6	v-rel reticuloendotheliosis viral or	328.9295	242	173.0443	248.1566	-9.27E-01	-4.40E-01	1	Unchanged Low
P19838	M15ef5	nuclear factor of kappa light poly	229.2262	277	173.0997	226.323	-4.05E-01	2.71E-01	1	Unchanged Low
Q92748	A24cd2	thyroid hormone responsive (SP1	101.3906	88.2	173.314	120.9562	7.73E-01	-2.02E-01	1	Unchanged Low
O95095	P13ab2	amyloid beta precursor protein (c	199.951	201	173.3314	191.35	-2.06E-01	5.88E-03	1	Unchanged Low
P52209	K18ab8	phosphoglucomutase dehydrogenase	211.8178	147	173.42	177.5327	-2.89E-01	-5.23E-01	1	Unchanged Low
P42566	H10ef5	epidermal growth factor receptor	194.9437	158	173.4643	175.3861	-1.68E-01	-3.05E-01	1	Unchanged Low
Q13772	D05gh6	nuclear receptor coactivator 4	273.5167	367	173.5038	271.4641	-6.57E-01	4.26E-01	1	Unchanged Low
P43897	D09gh6	Ts translation elongation factor:	325.7575	226	173.8484	241.8156	-9.06E-01	-5.28E-01	1	Unchanged Low
P09329	D08ef7	phosphoribosyl pyrophosphate s-	103.7682	86.2	174.5738	121.5057	7.50E-01	-2.65E-01	1	Unchanged Low
O75618	F24cd4	death effector domain-containing	172.0163	176	174.7689	174.3849	2.29E-02	3.61E-02	1	Unchanged Low
Q9UH9	B18ef1	flavohemoprotein b5+b5R	169.2028	197	174.7919	180.2862	4.69E-02	2.18E-01	1	Unchanged Low
Q9H824	J07gh6	F-box only protein 22	89.2751	161	175.62	141.9533	9.76E-01	8.50E-01	1	Unchanged Low
Q9UQ43	G07ab3	BA11-associated protein 2	184.8198	165	175.6399	175.1475	-7.35E-02	-1.64E-01	1	Unchanged Low
O43173	N08ef1	steryltransferase 8C (alpha2;3Ga	220.9909	256	175.9869	217.6266	-3.29E-01	2.12E-01	1	Unchanged Low
Q9BZ22	G13gh7	slaloadhesin	147.52	189	175.9952	170.7942	2.55E-01	3.56E-01	1	Unchanged Low
Q92611	I16gh1	KIAA0212 gene product	98.3144	94.3	176.0348	122.2108	8.70E-01	-3.08E-02	1	Unchanged Low
Q969V6	K14gh7	megakaryoblastic leukemia (van	135.6533	161	176.0531	157.6423	3.76E-01	2.49E-01	1	Unchanged Low
P08107	K14ab7	heat shock 70kD protein 1B	153.5141	106	176.1145	145.1219	1.98E-01	-5.38E-01	1	Unchanged Low
Q9BQ24	E21gh6	hypothetical protein MGCC2500	153.9741	255	176.3898	195.2182	1.95E-01	7.29E-01	1	Unchanged Low
Q9H7X1	N07gh5	hypothetical protein FLJ14153	155.291	236	176.5938	189.2619	1.85E-01	8.03E-01	1	Unchanged Low
Q99616	D09cd2	small inducible cytokine subfamily	130.1641	100	176.5958	135.6192	4.40E-01	-3.79E-01	1	Unchanged Low
Q92896	L04cd7	golgi apparatus protein 1	97.73429	90.3	176.622	121.5361	8.54E-01	-1.15E-01	1	Unchanged Low
Q14582	J16ef6	Mad4 homolog	210.3185	244	176.6383	210.1876	-2.52E-01	2.12E-01	1	Unchanged Low
Q13505	K21ab7	melanin 1	199.1231	168	176.6745	181.2437	-1.73E-01	-2.46E-01	1	Unchanged Low
Q13722	O24cd8	chromosome 3p21.1 gene seque	85.85963	144	176.7101	135.6336	1.04E+00	7.49E-01	1	Unchanged Low
P01308	H10ab6	Insulin	367.022	113	176.7437	218.8465	-1.05E+00	-1.70E+00	1	Unchanged Low
O00405	D19ab8	protein phosphatase 1; regulator	233.0866	306	176.8763	238.6383	-3.98E-01	3.92E-01	1	Unchanged Low
P41215	E03ab5	fatty-acid-Coenzyme A ligase; iso	267.9822	199	177.1301	214.8046	-5.97E-01	-4.27E-01	1	Unchanged Low
P31314	F04ef6	homeo box 11 (T-cell lymphoma	107.4127	170	177.4236	151.5175	7.24E-01	6.60E-01	1	Unchanged Low
O95427	G21cd8	phosphatidylinositol glycan class	84.22817	116	177.4629	125.8189	1.08E+00	4.59E-01	1	Unchanged Low
Q12981	B24ef6	BCI2/adenovirus E1B 19kD inte	62.38214	99.8	177.5246	119.9152	1.11E+00	2.77E-01	1	Unchanged Low
Q9Y5V1	L10ef1	HSPC042 protein	212.074	184	177.7635	191.3703	-2.55E-01	-2.03E-01	1	Unchanged Low
Q9H4B4	O22ab4	cytokine-inducible kinase	161.982	194	177.788	177.8629	1.34E-01	2.59E-01	1	Unchanged Low
Q9H601	P15gh5	chromosome 20 open reading frz	95.43432	108	177.8526	126.8312	6.98E-01	1.72E-01	1	Unchanged Low
O60504	J18cd5	Vinexin beta (SH3-containing ad	109.3831	99.8	177.8876	129.0088	7.02E-01	-1.33E-01	1	Unchanged Low
Q9UNIK0	I02cd5	synlaxin 8	218.2149	171	177.9777	189.0342	-2.94E-01	-3.53E-01	1	Unchanged Low
Q95657	B24cd4	proline-serine-threonine phospho	369.3485	158	178.0072	235.2956	-1.06E+00	-1.23E+00	1	Unchanged Low
P20645	C05ab7	mannose-6-phosphate receptor (	355.8249	234	178.1318	256.0667	-9.98E-01	-6.03E-01	1	Unchanged Low
O14569	B03ab2	putative tumor suppressor	122.4884	79.2	178.135	126.62	5.40E-01	-6.28E-01	1	Unchanged Low
O15293	D18cd3	MAP-kinase activating death dom	157.092	114	178.1577	149.8523	1.82E-01	-4.59E-01	1	Unchanged Low
P00390	E14ef7	glutathione reductase	282.1492	196	178.1741	218.8246	-6.63E-01	-5.24E-01	1	Unchanged Low
Q9HBV3	K24gh5	PP3111 protein	229.2714	361	178.4093	256.1517	-3.62E-01	6.54E-01	1	Unchanged Low
Q14558	H17ab8	phosphoribosyl pyrophosphate s-	301.2129	227	178.4567	235.5213	-7.55E-01	-4.09E-01	1	Unchanged Low
O14710	F01ef5	cell cycle progression 2 protein	261.2178	189	178.7923	209.7103	-5.47E-01	-4.66E-01	1	Unchanged Low
Q9UJ70	J10ef3	N-sacetylglucosamine kinase	151.2986	276	178.7992	201.9381	2.41E-01	8.66E-01	1	Unchanged Low
Q13397	M18cd6	zinc finger protein 238	215.883	285	178.9318	226.5893	-2.71E-01	4.00E-01	1	Unchanged Low
Q9NRG4	B21gh4	HSKM-B protein	143.1326	279	178.999	200.3335	3.23E-01	9.62E-01	1	Unchanged Low

P51449	B01cd2	RAR-related orphan receptor C	236.6977	97.2	179.0372	170.992	-4.03E-01	-1.28E+00	1	Unchanged Low
Q5H768	O21gh1	synaptotagmin-like 2	83.78255	121	179.0813	120.0355	1.10E+00	5.33E-01	1	Unchanged Low
Q14332	F22ef5	frizzled homolog 2 (Drosophila)	86.25011	129	179.1323	131.3078	1.05E+00	5.76E-01	1	Unchanged Low
Q13207	N13cd2	T-box 2	118.9378	108	179.1858	135.2524	5.91E-01	-1.44E-01	1	Unchanged Low
Q5H688	B19gh5	hypothetical protein similar to mc	134.338	129	179.5015	147.5119	4.18E-01	-6.19E-02	1	Unchanged Low
O00462	J09ab7	mannosidase; beta A; lysosomal	83.23817	107	179.6953	123.2365	1.11E+00	3.59E-01	1	Unchanged Low
Q9Y3D8	H14ef2	adrenal gland protein AD-004	178.4931	163	179.7989	173.7578	1.05E-02	-1.31E-01	1	Unchanged Low
P17900	F19ab3	GM2 ganglioside activator protein	124.7747	232	179.914	176.9056	5.28E-01	8.95E-01	1	Unchanged Low
Q9P0M4	O10cd8	Interleukin 17C	260.8753	223	180.0241	221.2511	-5.35E-01	-2.27E-01	1	Unchanged Low
	F13gh8	G protein-coupled receptor 54	87.92591	133	180.0735	133.5723	1.03E+00	5.94E-01	1	Unchanged Low
Q9NZ92	J02gh3	SWV/SNF related; matrix associa-	267.7307	247	180.206	231.4963	-5.71E-01	-1.19E-01	1	Unchanged Low
Q9NX94	L18gh6	hypothetical protein FLJ20154	133.6318	165	180.3424	159.7713	4.32E-01	3.07E-01	1	Unchanged Low
P04049	G12ef5	v-raf-1 murine leukemia viral onc	225.086	183	180.3925	196.2063	-3.19E-01	-2.98E-01	1	Unchanged Low
Q13181	B06cd1	ATP-binding cassette; sub-family	167.9383	127	180.4651	158.5133	1.04E-01	-4.02E-01	1	Unchanged Low
P22102	M05ab6	phosphoribosylglycinamide form	295.0489	180	180.5026	218.4202	-7.09E-01	-7.15E-01	1	Unchanged Low
Q9NCZ8	A09gh5	endothelial zinc finger protein Inc	96.79284	138	180.7283	138.4428	9.01E-01	5.10E-01	1	Unchanged Low
Q9JN30	D04cd2	sex comb on midleg-like 1 (Dros	97.47885	66	181.0121	121.4921	8.93E-01	-1.81E-01	1	Unchanged Low
P26651	J04ef6	zinc finger protein 36; C3H type;	286.0733	162	181.0638	209.8211	-6.60E-01	-8.17E-01	1	Unchanged Low
P18887	O06ef6	X-ray repair complementing factor 5	85.61601	102	181.0778	122.9254	1.08E+00	2.54E-01	1	Unchanged Low
Q9Y2S0	P14ef1	RNA polymerase I 16 kDa subun	182.9338	149	181.2184	170.8985	-1.36E-02	-3.00E-01	1	Unchanged Low
P49023	I05ef7	padilin	313.7788	334	181.2995	276.3491	-7.91E-01	9.00E-02	1	Unchanged Low
P49321	O03ab7	nuclear autoantigenic sperm prot	119.903	78.2	181.3524	126.4866	5.97E-01	-6.17E-01	1	Unchanged Low
Q13428	M14cd1	Treacher Collins-Franceschetti s	164.3621	123	181.4282	156.2838	4.43E-01	-4.18E-01	1	Unchanged Low
Q9HCS6	G07gh4	vacuolar protein sorting 11 (yeas	177.2833	302	181.4601	220.0848	3.36E-02	7.66E-01	1	Unchanged Low
P20813	I02gh6	cytochrome P450; subfamily IIb (	122.3562	162	181.476	155.3947	5.69E-01	4.08E-01	1	Unchanged Low
O00459	C05cd1	phosphoinositide-3-kinase; regul	145.3741	160	181.534	162.3275	3.20E-01	1.39E-01	1	Unchanged Low
P50151	H24ab4	guanine nucleotide binding prot	186.5329	193	182.0963	187.0796	-3.47E-02	4.62E-02	1	Unchanged Low
Q16850	D12ab3	cytochrome P450; 51 (lanosterol	353.9667	116	182.1309	217.3331	-9.59E-01	-1.61E+00	1	Unchanged Low
Q9ULW3	J09cd8	TATA-binding protein-binding pr	97.23454	207	182.1565	162.0616	9.06E-01	1.09E+00	1	Unchanged Low
Q16378	O20cd7	proline rich 4 (lactam)	81.91	152	182.3589	138.8678	1.15E+00	8.95E-01	1	Unchanged Low
P41240	J14ab4	c-src tyrosine kinase	175.1285	153	182.4257	170.0806	5.89E-02	-1.98E-01	1	Unchanged Low
Q16649	G05cd1	nuclear factor; Interleukin 3 regul	353.6698	169	182.4266	235.1072	-9.55E-01	-1.06E+00	1	Unchanged Low
Q9Y3M2	J03ef8	chromosome 22 open reading fra	74.27488	194	182.6022	150.2264	1.30E+00	1.38E+00	1	Unchanged Low
Q9UK58	M14gh4	cyclin L anla-6a	191.3619	313	182.6351	229.0134	-6.73E-02	7.10E-01	1	Unchanged Low
P47874	M23cd1	olfactory marker protein	250.3691	172	182.73	201.6274	-4.54E-01	-5.43E-01	1	Unchanged Low
O95620	O03cd7	protein similar to E.coli yhdg and	227.8932	207	183.1055	205.8925	-3.16E-01	-4.11E-01	1	Unchanged Low
Q9UHV2	J11cd8	CDK4-binding protein p34SE11	144.2806	163	183.5211	163.6559	3.47E-01	1.77E-01	1	Unchanged Low
P02810	F07gh6	proline-rich protein HaeIII subfam	410.3478	392	183.6977	328.6668	-1.16E+00	-6.62E-02	1	Unchanged Low
O94903	K04cd7	proline synthetase co-transcriber	242.2062	146	183.9744	190.7733	-3.97E-01	-7.29E-01	1	Unchanged Low
Q9PP0W6	I03ef4	lipopolysaccharide specific resp	149.1148	177	184.0725	169.9232	3.04E-01	2.43E-01	1	Unchanged Low
Q9HX4	O15gh5	stromal membrane-associated pr	358.1542	342	184.0879	294.6026	-9.60E-01	-6.84E-02	1	Unchanged Low
P02786	D24ef5	transferrin receptor (p90; CD71)	320.8365	257	184.2545	254.0696	-8.00E-01	-3.19E-01	1	Unchanged Low
E15ef1	Immunoglobulin heavy constant t	386.489	176	184.3533	249.0303	-1.07E+00	-1.13E+00	1	Unchanged Low	
MAD:	mothers against decapentap	227.5617	153	184.3978	188.4757	-3.04E-01	-5.69E-01	1	Unchanged Low	
Q15036	B23gh1	sorting nexin 17.	303.6909	411	184.4831	299.6453	-7.20E-01	4.34E-01	1	Unchanged Low
P31751	A08ab2	v-akt murine thymoma viral onco	253.7531	253	184.8245	230.4512	-4.57E-01	-5.57E-03	1	Unchanged Low
P11177	G21ab6	pyruvate dehydrogenase (liposo	229.1486	150	185.0719	188.1769	-3.08E-01	-6.08E-01	1	Unchanged Low
Q9UE6	F22ab2	arrestin; beta 2	190.7331	128	185.1221	167.9086	-4.31E-01	-5.77E-01	1	Unchanged Low
Q16531	J11ab5	damage-specific DNA binding pro	205.1934	229	185.1363	206.5357	-1.48E-01	1.60E-01	1	Unchanged Low
P28698	G24cd3	zinc finger protein 42 (myeloid-s	76.12612	105	185.3347	122.3029	1.28E+00	4.70E-01	1	Unchanged Low
P41968	N12ef4	melanocortin 3 receptor	225.3987	287	185.5363	232.6783	-2.81E-01	3.49E-01	1	Unchanged Low
P54920	E03cd4	N-ethylmaleimide-sensitive factor	306.753	267	185.697	252.9933	-7.24E-01	-2.03E-01	1	Unchanged Low
Q99487	C19ab8	platelet-activating factor acetyl	228.4138	241	185.7091	218.5222	-2.99E-01	8.00E-02	1	Unchanged Low
Q9HC8	N15gh7	integrin-linked kinase-associated	120.8459	109	185.7532	138.517	6.20E-01	-1.49E-01	1	Unchanged Low
P17252	F17ab8	protein kinase C; alpha	108.3851	74	185.8466	122.7553	7.78E-01	-5.50E-01	1	Unchanged Low
P04933	B01ef5	cell division cycle 2; G1 to S and	108.1696	76.2	185.8754	213.4207	7.81E-01	-5.05E-01	1	Unchanged Low
O00139	C14ab7	kinase heavy chain member 2	140.4141	205	185.9437	177.1988	4.05E-01	5.48E-01	1	Unchanged Low
P54259	N05ef6	dental/orbital-pallidolysian atrof	165.5295	152	186.0962	167.773	1.69E-01	-1.26E-01	1	Unchanged Low
Q9757	G10cd8	thioredoxin 2	309.0415	163	186.106	219.4587	-7.32E-01	-9.21E-01	1	Unchanged Low
Q9NW68	B12gh2	hypothetical protein FLJ10276	107.4044	242	186.1575	178.6551	7.93E-01	1.17E+00	1	Unchanged Low
P16106	O16gh6	H3 histone family; member J	137.9914	135	186.2589	152.9203	4.33E-01	-3.69E-02	1	Unchanged Low
P40692	M06ef6	muL homolog 1; colon cancer; n	98.77988	108	186.2872	131.0441	9.15E-01	1.30E-01	1	Unchanged Low
Q99798	E01ab2	aconitase 2; mitochondrial	615.211	291	186.5524	364.1757	-1.72E+00	-1.08E+00	1	Unchanged Low
P53618	A11ef3	coatomer protein complex; subunit	238.4951	102	186.5626	175.716	-3.54E-01	-1.23E+00	1	Unchanged Low
Q9UJ69	N24gh2	Toll-interacting protein	211.4055	259	186.6408	219.0188	-1.80E-01	2.93E-01	1	Unchanged Low
Q9NRM2	P22ef8	zinc finger protein 277	232.9567	227	186.8854	215.6334	-3.18E-01	-3.70E-02	1	Unchanged Low
Q92879	B06cd6	CUG triplet repeat; RNA binding	217.3752	198	187.122	200.6744	-2.16E-01	-1.38E-01	1	Unchanged Low
O75399	H22gh1	deformed epidermal autoregula	189.8387	266	187.2872	214.4669	-1.95E-02	4.88E-01	1	Unchanged Low
Q9BZE4	I17cd8	G protein-binding protein CRFG	151.2547	214	187.3094	184.3092	3.08E-01	5.03E-01	1	Unchanged Low
Q9NKB2	G08gh2	hypothetical protein FLJ20343	259.0672	285	187.4246	243.8822	-4.57E-01	1.38E-01	1	Unchanged Low
O95424	M05ef4	MYLE protein	103.2077	184	187.5574	158.2861	8.62E-01	8.35E-01	1	Unchanged Low
P54577	D14cd3	tyrosyl-tRNA synthetase	145.5748	108	187.5758	146.9084	3.66E-01	-4.36E-01	1	Unchanged Low
O43692	N03ef7	protease inhibitor 15	102.5299	163	187.7565	150.9471	8.73E-01	6.65E-01	1	Unchanged Low
O60507	J03cd3	tyrosyl/protein sulfotransferase 1	190.271	136	188.0843	171.4862	-1.67E-02	-4.83E-01	1	Unchanged Low
Q9BY59	B15gh5	MMS19-like (MET18 homolog); S	99.29429	117	188.1003	134.7877	9.22E-01	2.36E-01	1	Unchanged Low
P32780	G11ab6	general transcription factor IIIb; p	258.9396	180	188.3175	209.0492	-4.59E-01	-5.25E-01	1	Unchanged Low
Q14004	D07ef5	cell division cycle 2-like 5 (cholin	92.56943	158	188.3566	146.1954	1.02E+00	7.58E-01	1	Unchanged Low
Q15910	L08ab5	enhancer of zeste homolog 2 (Dr	213.1801	306	188.8314	235.9636	-1.75E-01	5.21E-01	1	Unchanged Low
P47974	H22ab4	zinc finger protein 36; C3H type-I	187.7102	163	188.8801	179.8162	8.96E-03	-2.05E-01	1	Unchanged Low
Q13177	E20ab8	p21 (CDKN1A)-activated kinase	367.7706	232	188.9048	262.9597	-9.61E-01	-6.63E-01	1	Unchanged Low
P16gh8	baculoviral IAP repeat-containing	251.3679	126	189.0052	188.6409	-4.11E-01	-1.00E+00	1	Unchanged Low	
P98172	J01ef7	ephrin-B1	122.68826	109	189.5198	140.4039	6.25E-01	-1.75E-01	1	Unchanged Low
Q9BQB1	N04gh6	hypothetical protein FLJ10342	113.906	172	189.7648	158.4309	7.35E-01	5.91E-01	1	Unchanged Low
O75472	H11cd5	DnaJ (Hsp40) homolog; subfamil	227.1041	204	189.9354	206.8756	-2.58E-01	-1.58E-01	1	Unchanged Low
O75608	K06cd6	lysophospholipase I	357.6112	374	190.1833	307.2824	-9.11E-01	6.48E-02	1	Unchanged Low
O00193	E14ef3	small acidic protein	223.9793	284	190.2397	232.7223	-2.36E-01	3.42E-01	1	Unchanged Low

Q14452	B08ab5	glucocorticoid receptor DNA blnc	156.8451	147	190.439	164.6255	2.80E-01	-9.75E-02	1	Unchanged Low
P55268	P18ef6	laminin; beta 2 (laminin S)	125.0717	152	190.5787	155.8763	6.08E-01	2.81E-01	1	Unchanged Low
Q5P006	A20ef8	mitochondrial ribosomal protein l	114.6952	151	190.6578	152.1556	7.33E-01	3.98E-01	1	Unchanged Low
Q5Y3B5	P07ef1	CGI-111 protein	158.6983	176	190.6804	175.2557	2.65E-01	1.52E-01	1	Unchanged Low
Q9NQ34	A10gh4	chromosome 11 open reading fr	144.3438	161	190.6944	165.3815	4.02E-01	1.59E-01	1	Unchanged Low
Q9NWY4	O14gh2	hypothetical protein FLJ20534	70.02507	110	191.0561	123.5579	1.45E+00	6.48E-01	1	Unchanged Low
Q9UBS4	P17eb2	ring finger protein 14	227.9827	247	191.1542	221.9109	-2.54E-01	1.13E-01	1	Unchanged Low
Q9UBS4	J06ef2	DnaJ (Hsp40) homolog; subfamI	181.8446	175	191.2168	182.7428	7.25E-02	-5.40E-02	1	Unchanged Low
Q12797	J22ab2	aspartate beta-hydroxylase	101.2251	86.5	191.3988	126.3618	9.19E-01	-2.27E-01	1	Unchanged Low
Q5H4H9	P10gh8	hypothetical gene supported by /	167.5049	219	191.4831	192.7601	1.93E-01	3.89E-01	1	Unchanged Low
O14907	E24ef8	Tax Interaction protein 1	351.7729	403	191.7684	315.6313	-8.75E-01	1.97E-01	1	Unchanged Low
Q14673	B09gh1	Bcl-2-associated transcription fac	97.16912	117	191.9499	135.533	9.82E-01	2.74E-01	1	Unchanged Low
Q9NW87	P01gh2	estrogen-related receptor beta II	567.7076	84.6	192.0982	281.455	-1.56E+00	-2.75E+00	1	Unchanged Low
Q9BVH4	G21gh6	hypothetical protein MGC3196	164.8572	169	192.4133	175.4765	2.23E-01	3.72E-02	1	Unchanged Low
P22897	I17ab7	mannose receptor; C type 1	77.30638	100	192.4612	123.4215	1.32E+00	3.78E-01	1	Unchanged Low
P19012	L04ab6	keratin 15	146.5632	130	192.6097	156.5003	3.94E-01	-1.69E-01	1	Unchanged Low
Q14738	C16cd1	protein phosphatase 2; regulator	224.4642	183	192.7984	200.124	-2.19E-01	-2.94E-01	1	Unchanged Low
O95152	F04cd4	vesicle trafficking protein	197.6319	195	192.9314	195.3686	-3.47E-02	-1.53E-02	1	Unchanged Low
P78426	A09cd3	NK6 transcription factor homolog	198.5291	353	193.0203	248.2544	-4.06E-02	8.31E-01	1	Unchanged Low
Q14797	P14ab3	caspase 8; apoptosis-related cys	124.8603	284	193.1013	200.6718	6.29E-01	1.19E+00	1	Unchanged Low
P07711	N13ab4	cathepsin L	137.16	121	193.1454	150.5861	4.94E-01	-1.75E-01	1	Unchanged Low
P32942	B02ab6	intercellular adhesion molecule 3	140.3673	140	193.1656	157.6897	4.61E-01	-8.57E-03	1	Unchanged Low
	L18ab2	ATPase; Na+K+ transporting; atp	188.9371	131	194.2503	171.3764	4.00E-02	-5.29E-01	1	Unchanged Low
Q9NW0	F13gh2	hypothetical protein FLJ20643	81.29108	107	194.4652	127.6547	1.26E+00	3.99E-01	1	Unchanged Low
Q9NW25	O05gh2	undine kinase-like 1	176.188	358	194.4782	242.9739	4.42E-01	1.02E+00	1	Unchanged Low
O75792	D15cd6	ribonuclease HI; large subunit	100.3515	99.6	194.705	131.5441	9.56E-01	-1.12E-02	1	Unchanged Low
P05141	I04ab2	solute carrier family 25 (mitochor	454.9832	311	194.7577	320.3918	-1.22E+00	-5.47E-01	1	Unchanged Low
Q9NX38	K22gh2	hypothetical protein FLJ20457	140.7383	161	195.2688	165.7012	4.72E-01	1.95E-01	1	Unchanged Low
Q9Y682	A18cd8	sec22 homolog	193.7656	271	195.3918	220.1941	1.21E-02	4.86E-01	1	Unchanged Low
P78381	C02cd4	solute carrier family 35 (UDP-gal	276.1692	207	195.6585	226.4009	-4.97E-01	4.14E-01	1	Unchanged Low
Q9UJMP5	B23ef3	replication initiation region protel	270.4297	179	195.6957	214.9641	-4.67E-01	-5.97E-01	1	Unchanged Low
Q9P0Q0	C15ef3	hypothetical protein HSPC228	129.6054	241	195.7376	188.838	5.95E-01	8.96E-01	1	Unchanged Low
Q9UJBQ3	M12cd7	polyamine-modulated factor 1	189.4397	172	195.7465	185.7473	4.72E-02	-1.39E-01	1	Unchanged Low
P27540	D22ab2	aryl hydrocarbon receptor nucleo	239.4814	258	195.7776	231.071	-2.91E-01	1.07E-01	1	Unchanged Low
Q9Y2W1	F03od5	thyroid hormone receptor-associ	160.2008	248	195.7777	201.323	2.89E-01	6.30E-01	1	Unchanged Low
P82267	E15ab5	adaptor-related protein complex	198.6022	231	195.7793	208.571	-2.07E-02	2.20E-01	1	Unchanged Low
P00918	C16ab3	carbonic anhydrase II	283.4506	172	195.9099	216.9569	-5.33E-01	-7.25E-01	1	Unchanged Low
Q9Y663	E07cd6	heparan sulfate (glucosamine) 3-	259.052	99.6	196.1045	184.9847	-4.02E-01	-1.38E+00	1	Unchanged Low
Q9NX40	K18gh2	ovarian carcinoma immunoreacti	119.6155	247	196.1836	187.7108	7.14E-01	1.05E+00	1	Unchanged Low
P50222	L09ab7	mesenchyme homeo box 2 (grow	165.3048	223	196.5502	195.0839	2.50E-01	4.34E-01	1	Unchanged Low
Q13610	C16cd7	nuclear phosphoprotein similar to	160.8948	331	196.7055	229.4375	2.90E-01	1.04E+00	1	Unchanged Low
P49591	B12cd2	serly-IRNA synthetase	152.5268	69.6	196.7944	139.6467	3.68E-01	-1.13E+00	1	Unchanged Low
P04554	C19gh5	prolamine 3	314.8934	296	196.9835	269.3189	-6.77E-01	-8.89E-02	1	Unchanged Low
P02538	N12ef6	keratin 6A	227.8925	277	197.1759	233.9139	-2.09E-01	2.80E-01	1	Unchanged Low
Q13637	G23cd7	RAB32; member RAS oncogene	392.0158	269	197.2609	286.1382	-9.91E-01	-5.43E-01	1	Unchanged Low
P39086	J02ab3	glutamate receptor; ionotropic; k	184.3318	210	197.334	197.2285	9.83E-01	1.88E-01	1	Unchanged Low
Q9HF9	H20gh5	hypothetical protein 24432	287.08	202	197.402	228.8927	-5.40E-01	-5.06E-01	1	Unchanged Low
Q99460	L13ab8	proteasome (prosome; macropal	298.3527	228	197.4025	242.122	-5.96E-01	-3.89E-01	1	Unchanged Low
Q9UKP6	D20gh1	G protein-coupled receptor 14	213.3717	142	197.5131	184.3366	-1.11E-01	-5.86E-01	1	Unchanged Low
Q16589	A04ef5	cyclin G2	99.61434	214	197.5658	170.3526	9.88E-01	1.10E+00	1	Unchanged Low
O95316	M03cd5	ribosomal protein S6 kinase; 90k	144.8234	145	197.5662	162.3224	4.48E-01	-2.40E-03	1	Unchanged Low
O14545	A09cd7	FLN29 gene product	238.4292	288	197.8936	241.5146	-2.69E-01	2.74E-01	1	Unchanged Low
Q9Y249	P03cd6	homologous to yeast nitrogen pe	191.1146	224	198.1049	204.4863	5.18E-02	2.31E-01	1	Unchanged Low
Q92794	K12cd4	zinc finger protein 220	134.123	179	198.312	170.3523	5.64E-01	4.13E-01	1	Unchanged Low
P36894	A12ab3	bone morphogenic protein rece	149.2953	236	198.4963	194.5153	4.11E-01	6.59E-01	1	Unchanged Low
P79525	L21ab7	MHC class I polypeptide-related	120.8289	125	198.5782	148.0291	7.17E-01	4.53E-02	1	Unchanged Low
O14947	K04ab6	laminin; beta 3 (necine 125kD);	360.8887	284	198.2636	281.2972	-8.57E-01	-3.47E-01	1	Unchanged Low
Q12899	K16cd3	tripartite motif-containing 26	188.6935	250	199.2998	212.5994	7.89E-02	4.05E-01	1	Unchanged Low
	M24gh8	zinc finger protein 289; ID1 regul	91.37228	137	199.4969	142.4645	1.13E+00	5.79E-01	1	Unchanged Low
Q9UIJ5	A18ef2	zinc finger; DHHC domain contai	436.5048	452	199.696	362.7132	-1.13E+00	5.01E-02	1	Unchanged Low
P46821	J11ab7	microtubule-associated protein 1	121.2356	136	199.8286	152.4972	7.21E-01	1.70E-01	1	Unchanged Low
O60906	P04cd1	sphingomyelin phospholipidase	282.5771	281	199.835	254.5351	-5.00E-01	-7.08E-03	1	Unchanged Low
P04040	O18ab5	catalase	160.7098	239	199.9293	199.8034	3.15E-01	5.71E-01	1	Unchanged Low
O60709	B16cd5	dynamin 1-like	85.33527	220	199.9492	168.4792	1.23E+00	1.37E+00	1	Unchanged Low
Q14714	A02cd4	sarcospan (Kras oncogene-assoc	376.724	148	200.1413	242.1468	-9.20E-01	-1.36E+00	1	Unchanged Low
P39687	F01cd4	acidic (leucine-rich) nuclear pha	226.8272	108	200.186	178.3873	-1.80E-01	-1.07E+00	1	Unchanged Low
O75341	K16cd4	BRCA1 associated protein	151.895	209	200.2666	187.1088	3.99E-01	4.62E-01	1	Unchanged Low
Q9NUH5	D16gh3	hypothetical protein FLJ11259	152.5767	196	200.5435	182.989	3.94E-01	3.60E-01	1	Unchanged Low
Q9UHR5	L22ef7	transcriptional regulator protein	225.1172	345	200.7483	256.9591	-1.65E-01	6.16E-01	1	Unchanged Low
Q9UMX3	D15gh8	BCL2-related ovarian killer	185.2616	176	200.8587	187.4707	1.16E-01	-7.26E-02	1	Unchanged Low
Q02297	J05ef6	neuregulin 1	89.51288	234	201.3025	175.0464	1.17E+00	1.39E+00	1	Unchanged Low
Q9BQ83	A21gh6	hypothetical protein MGC5178	302.7768	398	201.3498	300.7124	-5.89E-01	3.95E-01	1	Unchanged Low
O43491	C22ab4	erythrocyte membrane protein bz	265.5557	144	201.5206	203.6633	-3.98E-01	-8.84E-01	1	Unchanged Low
Q92922	N16cd1	SWISS-PROT related; matrix associ	251.3134	195	201.571	216.0309	-3.18E-01	-3.64E-01	1	Unchanged Low
Q16099	J11ef3	glutamate receptor; ionotropic; k	200.0311	288	201.66	229.9201	1.17E-02	5.26E-01	1	Unchanged Low
O95328	B06gh4	hypothetical protein 628	253.2751	240	201.6969	231.7377	3.28E-01	-7.56E-02	1	Unchanged Low
Q06265	C15cd1	polymyositis/scleroderma autoan	167.3169	182	202.2097	183.9827	2.73E-01	1.25E-01	1	Unchanged Low
Q01780	K12gh6	polymyositis/scleroderma autoa	196.9508	270	202.2308	223.1866	3.82E-02	4.57E-01	1	Unchanged Low
Q9NP9	G07ef3	HeLa cyclin-dependent kinase 2	251.6953	170	202.5242	207.9337	-3.14E-01	5.70E-01	1	Unchanged Low
Q9P110	B03ef4	zinc ribbon domain containing; 1	110.7474	151	202.7351	154.8483	8.72E-01	4.48E-01	1	Unchanged Low
O13480	C02ab5	GRB2-associated binding protein	171.5634	150	203.065	174.7357	2.43E-01	-1.98E-01	1	Unchanged Low
O95205	O05gh1	C3H-type zinc finger protein; sim	136.7838	267	203.3797	202.2261	5.72E-01	9.62E-01	1	Unchanged Low
O76091	I11cd1	nitinase 1	194.24	179	203.4317	192.2638	8.67E-02	-1.17E-01	1	Unchanged Low
Q9Y364	F21ef2	DKFZP434J154 protein	208.15	322	203.5516	244.4561	-3.22E-02	6.28E-01	1	Unchanged Low
P51116	I14cd5	fragile X mental retardation; auto	215.9784	213	203.6388	210.8166	-8.49E-02	-2.12E-02	1	Unchanged Low
P49915	H19cd4	guanine monophosphate syntheta	175.5001	115	203.6534	164.8237	2.15E-01	-6.13E-01	1	Unchanged Low

Q9UHR3	O04cd8	nasopharyngeal carcinoma susceptibility protein	120.0173	196	203.8212	173.3257	7.64E-01	7.09E-01	1	Unchanged	Low
Q15007	O10cd5	Wilms' tumour 1-associated protein	237.1077	258	204.226	233.0967	-2.15E-01	1.22E-01	1	Unchanged	Low
P24941	B03ef4	cyclin-dependent kinase 2	98.60804	214	204.3554	172.2468	1.05E+00	1.12E+00	1	Unchanged	Low
P53634	L01ef7	calhepsin C	97.3314	77.9	204.771	126.6548	1.07E+00	-3.22E-01	1	Unchanged	Low
Q13123	K03ef7	IK cytokine; down-regulator of Ht	108.6134	153	204.9565	155.5636	9.16E-01	4.95E-01	1	Unchanged	Low
Q9NUT6	P21gh3	hypothetical protein FLJ11151	285.3106	565	205.0218	351.7208	-4.77E-01	9.85E-01	1	Unchanged	Low
Q9Y279	B23cd7	Ig superfamily protein	356.8489	226	205.0368	262.6019	-7.99E-01	-6.59E-01	1	Unchanged	Low
Q75319	H07cd3	dual specificity phosphatase 11 (	250.2151	205	205.1456	220.2678	-2.87E-01	-2.84E-01	1	Unchanged	Low
Q9NYH9	L08ef3	hepatocellular carcinoma-associated protein	267.2586	283	205.223	258.6032	-4.85E-01	-1.99E-02	1	Unchanged	Low
Q9UNF0	M20cd7	protein kinase C and casein kinase	438.5503	349	205.53	331.0599	-1.09E+00	-3.29E-01	1	Unchanged	Low
O60437	D03ab5	periplakin	443.9882	301	205.5879	316.8358	-1.11E+00	-5.61E-01	1	Unchanged	Low
Q9NZN8	N22cd8	CCR4-NOT transcription complex	189.665	224	205.673	266.5153	1.17E-01	2.41E-01	1	Unchanged	Low
Q14232	A18ab4	eukaryotic translation initiation factor 4A	273.7271	210	205.7436	229.9659	-4.12E-01	-3.79E-01	1	Unchanged	Low
O00142	C03ef5	thymidine kinase 2; mitochondrial	124.7128	147	205.9951	159.1674	7.24E-01	2.35E-01	1	Unchanged	Low
O60443	N16ab5	deafness; autosomal dominant 15	122.4035	284	206.3187	197.4327	7.53E-01	1.11E+00	1	Unchanged	Low
O95406	J20cd5	cornichon-like protein	181.7181	138	206.4442	175.4375	1.84E-01	-3.95E-01	1	Unchanged	Low
Q12841	E24cd7	follistatin-like 1	80.93058	97.7	206.5097	128.3877	1.35E+00	2.72E-01	1	Unchanged	Low
O15217	B04ab5	glutathione S-transferase A4	78.38055	91.3	206.6118	125.424	1.40E+00	2.20E-01	1	Unchanged	Low
P10645	E01ab4	chromogranin A (parathyroid secretory protein)	115.7467	283	206.8714	201.8992	8.38E-01	1.29E+00	1	Unchanged	Low
Q9HA66	D09gh5	G protein beta subunit-like protein	198.1992	192	206.9573	199.1923	6.24E-02	-2.47E-02	1	Unchanged	Low
Q9Y439	B08ef8	PRP31 pre-mRNA processing factor	175.7234	310	207.0904	230.9065	2.37E-01	6.19E-01	1	Unchanged	Low
Q9Y386	G08ef2	CG-78 protein	325.6509	246	207.7702	259.7061	-6.48E-01	-4.06E-01	1	Unchanged	Low
P53990	D21gh1	KIAA0174 gene product	230.1187	401	207.9831	279.676	-1.48E-01	8.01E-01	1	Unchanged	Low
O95865	O11ef3	dimethylarginine dimethylaminohydrolase	125.0105	157	208.0048	163.3476	7.35E-01	3.29E-01	1	Unchanged	Low
B21ef1		immunoglobulin lambda heavy chain polypeptide	142.7367	230	208.1338	193.5142	5.44E-01	6.66E-01	1	Unchanged	Low
Q15834	H17cd7	hepatitis delta antigen-interacting protein	320.7647	226	208.1753	251.6031	-6.24E-01	-5.06E-01	1	Unchanged	Low
P18846	H05ab4	activating transcription factor 1	470.9776	206	208.3404	295.2222	-1.18E+00	-1.19E+00	1	Unchanged	Low
Q14349	A23cd7	HLA-B associated transcript 8	138.8938	175	208.5984	174.3142	5.87E-01	3.37E-01	1	Unchanged	Low
Q9NV5M	M08gh3	hypothetical protein FLJ10637	98.19923	115	209.0315	140.794	1.09E+00	2.30E-01	1	Unchanged	Low
P12955	N18ab7	peptidase D	133.8157	192	209.0325	178.2382	6.43E-01	5.20E-01	1	Unchanged	Low
Q99700	D14cd1	spinocerebellar atrophy 2 (olivopontocerebellar atrophy)	191.0044	240	209.0555	213.1956	1.30E-01	3.27E-01	1	Unchanged	Low
Q9UJA2	E21gh3	chromosome 20 open reading frame	134.2553	316	209.2227	219.8275	6.40E-01	1.23E+00	1	Unchanged	Low
Q02246	J21ef6	contactin 2 (axonal)	108.0043	68.8	209.3915	128.7469	9.55E-01	-6.50E-01	1	Unchanged	Low
P48553	E06cd2	transmembrane protein 1	148.0375	238	209.4168	198.4177	5.00E-01	6.84E-01	1	Unchanged	Low
Q99639	K03cd2	suppressor of Ty 5 homolog (S. cerevisiae)	225.1962	296	209.795	243.5051	-1.02E+00	3.92E-01	1	Unchanged	Low
Q9NOX5	N02gh4	neural proliferation/differentiation factor	188.0695	206	209.8245	201.225	1.58E-01	1.30E-01	1	Unchanged	Low
Q99799	O08cd6	nuclear RNA export factor 1	205.4132	175	209.9237	196.7655	3.13E-02	-2.32E-01	1	Unchanged	Low
Q9BZV1	J05gh7	UBX domain-containing 1	127.7069	236	209.9733	191.2074	7.17E-01	8.86E-01	1	Unchanged	Low
Q03113	M19ab5	guanine nucleotide binding protein	140.2412	112	209.9975	154.1344	5.82E-01	-3.22E-01	1	Unchanged	Low
P01130	B21ab6	low density lipoprotein receptor	301.1179	394	210.369	301.7776	-5.17E-01	3.87E-01	1	Unchanged	Low
Q9UHN6	L11cd8	transmembrane protein 2	182.3012	130	210.5088	174.2344	2.08E-01	-4.89E-01	1	Unchanged	Low
Q99738	A03cd3	pinin; desmosome associated protein	200.7164	204	210.6944	205.0214	7.00E-02	2.10E-02	1	Unchanged	Low
Q9Y576	N03ef2	ankyrin repeat and SOCS box-cc	121.1139	76.2	210.8608	136.0527	8.00E-01	-6.69E-01	1	Unchanged	Low
P02304	B03gh6	H4 histone family 2	81.15302	191	210.8651	161.1408	1.38E+00	1.24E+00	1	Unchanged	Low
P01118	I08ab7	v-Ki-ras2 Kirsten rat sarcoma 2 v	209.4177	239	211.0234	219.9522	1.10E-02	1.93E-01	1	Unchanged	Low
P15924	K13ef7	desmoplakin (DPI; DP1)	249.9083	263	211.0334	241.3619	-2.44E-01	7.48E-02	1	Unchanged	Low
O43597	A19cd6	sprouty homolog 2 (Drosophila)	119.5051	155	211.0573	161.8627	8.21E-01	3.75E-01	1	Unchanged	Low
P09622	L06ab3	dihydrofolate dehydrogenase	346.3029	232	211.1679	263.2128	-7.14E-01	-5.77E-01	1	Unchanged	Low
Q08257	G16ef7	crystallin; zeta (quinone reductase)	514.6998	301	211.8448	342.4639	-1.28E+00	-7.73E-01	1	Unchanged	Low
Q9UHY8	J09cd7	fasculinization and elongation protein	86.8735	95.1	211.8571	131.2705	1.29E-01	1.31E-01	1	Unchanged	Low
P10646	P23cd2	tissue factor pathway inhibitor 1 (I)	596.8869	458	212.0146	422.403	-1.49E+00	-3.81E-01	1	Unchanged	Low
Q92685	L08cd5	Not56 (D. melanogaster)-like protein	195.2017	217	212.2397	208.1394	1.21E-01	1.53E-01	1	Unchanged	Low
P34949	I13ab7	mannose phosphate isomerase	102.2281	135	212.3424	149.8251	1.05E+00	4.00E-01	1	Unchanged	Low
Q9NP9	M21ef8	SPHC55 protein	91.56792	157	212.3544	153.7649	1.21E+00	7.81E-01	1	Unchanged	Low
Q99853	J24ef7	forkhead box B1	141.4272	105	212.4773	153.0918	5.87E-01	-4.25E-01	1	Unchanged	Low
Q9HD41	C24gh4	CHMP1.5 protein	280.2988	230	212.8608	241.047	-3.97E-01	-2.85E-01	1	Unchanged	Low
Q16625	A10ab8	occludin	859.5688	338	212.9222	470.2634	-2.01E+00	-1.35E+00	1	Unchanged	Low
P45973	L18ef6	chromobox homolog 5 (HP1 alpha)	164.9514	124	213.1315	167.3186	3.70E-01	-4.13E-01	1	Unchanged	Low
Q9NV19	O12gh3	hypothetical protein FLJ10707	136.0971	136	213.1484	161.8885	6.47E-01	3.42E-03	1	Unchanged	Low
P37173	O09ef7	transforming growth factor, beta 1	112.4415	208	213.3211	178.0584	9.24E-01	8.90E-01	1	Unchanged	Low
Q9UKF7	O21cd8	retinal degeneration B beta	333.6061	287	213.5389	277.9863	-6.44E-01	-2.18E-01	1	Unchanged	Low
P16870	J23ef7	carboxypeptidase E	81.85341	137	213.5973	144.0377	1.38E+00	7.40E-01	1	Unchanged	Low
P00374	D16ab3	dihydrofolate reductase	148.8142	59.6	213.6217	140.6638	5.22E-01	-1.32E+00	1	Unchanged	Low
P19957	M04ab8	protease inhibitor 1; skin-derived	202.9357	582	213.9068	333.0661	7.60E-02	1.52E+00	1	Unchanged	Low
O75962	J24cd2	tripe functional domain (PTPRF)	233.7849	197	213.9409	215.0154	-1.28E-01	-2.45E-01	1	Unchanged	Low
P16050	C24ab2	arachidonate 15-lipoxygenase	268.5504	87.3	213.9824	196.6194	4.31E-01	-1.72E+00	1	Unchanged	Low
Q9Y3D2	M11cd7	pili-like transcription factor	200.9397	224	214.0069	213.0068	9.09E-02	1.57E-01	1	Unchanged	Low
O00505	J18ab6	karyopherin alpha 3 (importin alpha 3)	358.8945	313	214.0819	295.4165	-7.45E-01	-1.96E-01	1	Unchanged	Low
Q9NZD8	N15ef1	adducin cluster protein 33	222.816	223	214.2968	220.0079	-5.62E-02	6.21E-04	1	Unchanged	Low
P46937	G10cd6	Yos-associated protein 1; 65 kDa	219.0427	268	214.3846	233.924	-3.10E-02	2.93E-01	1	Unchanged	Low
P53384	O05ab7	nucleoloid binding protein 1 (Min)	272.4995	223	214.5051	236.5867	-3.45E-01	-2.91E-01	1	Unchanged	Low
Q9UI28	K10ef4	AD-003 protein	120.4634	147	214.7067	160.6424	8.34E-01	2.84E-01	1	Unchanged	Low
Q14651	O20ab8	plastin 1 (I Isoform)	517.7448	303	214.7993	345.2493	-1.27E+00	-7.72E-01	1	Unchanged	Low
P10914	K01ef6	interferon regulatory factor 1	310.6599	395	214.9514	308.8604	-5.32E-01	3.46E-01	1	Unchanged	Low
P21281	A03ab3	ATPase; H <sup>+</sup> transporting; lysosomal	299.07	638	215.0012	383.914	-4.76E-01	1.09E+00	1	Unchanged	Low
P53701	G19ab6	holocytochrome c synthase (cytochrome c oxidase)	251.8825	415	215.1177	293.8903	-2.28E-01	7.19E-01	1	Unchanged	Low
Q9Y2B1	C18ef3	transmembrane protein 5	103.4737	123	215.2492	147.2535	1.05E+00	2.50E-01	1	Unchanged	Low
Q14166	D23ef8	KIAA0153 protein	332.5834	276	215.4485	274.7657	-8.26E-01	-2.68E-01	1	Unchanged	Low
Q15738	B09ef4	NAD(P) dependent steroid dehydrogenase	253.061	171	215.5558	213.0647	-2.31E-01	-5.69E-01	1	Unchanged	Low
Q16586	I08cd1	sarcoglycan; alpha (50kD dystroglycan)	356.2221	128	215.8058	234.3661	-7.31E-01	-1.47E+00	1	Unchanged	Low
Q9Y6J8	L05ef2	magainin phospholipase-like protein	275.0054	326	215.9987	272.4953	-3.46E-01	2.48E-01	1	Unchanged	Low
Q9HF52	P17gh5	hypothetical protein FLJ23499	204.1242	332	216.1178	250.8425	8.24E-02	7.03E-01	1	Unchanged	Low
Q05655	E02cd1	protein kinase C; delta	419.7056	297	216.1184	310.8344	-9.58E-01	-5.00E-01	1	Unchanged	Low
Q9NXU7	M03gh3	hypothetical protein FLJ20048	240.4802	235	216.1338	230.6008	-1.54E-01	-3.21E-02	1	Unchanged	Low
Q15498	P21cd6	SNARE protein Ykl6	188.9561	242	216.7243	215.7355	1.98E-01	3.54E-01	1	Unchanged	Low
Q9266											

Q9Y223	N03cd5	UDP-N-acetylglucosamine-2-epfr	207.311	295	217.1156	239.9617	6.67E-02	5.11E-01	1	Unchanged Low
Q95816	E21ab3	BCL2-associated athanogene 2	84.7224	94.2	217.4827	132.1461	1.36E+00	1.53E-01	1	Unchanged Low
Q9H40K5	A21gh8	hypothetical protein DKFZp434H	193.1934	324	217.6924	244.8706	1.72E-01	7.45E-01	1	Unchanged Low
Q9BTJ1	C03e2	ribosomal protein S27-like	132.1497	411	218.2702	253.7125	7.24E-01	1.84E+00	1	Unchanged Low
Q9NRR5	J23gh4	chromosome 1 open reading frar	138.2192	201	218.4149	185.8791	6.60E-01	5.40E-01	1	Unchanged Low
Q9Y5L3	A13ab4	ectonucleoside triphosphate diph	235.2745	316	218.4547	256.4569	-1.07E-01	4.24E-01	1	Unchanged Low
Q75351	K06cd5	suppressor of K+ transport defec	274.5936	311	218.6389	267.9692	-3.29E-01	1.78E-01	1	Unchanged Low
Q75443	F07cd2	lectin alpha	163.4591	150	218.7282	184.2202	2.54E-01	-2.86E-01	1	Unchanged Low
Q9H7X4	K04gh7	KIAA1085 protein	268.2576	372	218.7527	286.2489	-2.94E-01	4.71E-01	1	Unchanged Low
Q00255	K22ab6	multiple endocrine neoplasia I	134.7209	117	218.9335	156.9374	7.01E-01	-2.02E-01	1	Unchanged Low
Q9BV94	D05gh3	chromosome 20 open reading frar	319.259	316	219.2324	284.912	-5.42E-01	-1.37E-02	1	Unchanged Low
O14813	O10ab2	airless homeobox ( <i>Drosophila</i> )	226.3067	320	219.2567	255.131	-4.57E-02	4.99E-01	1	Unchanged Low
P35269	D15ab4	general transcription factor IIIF; p	243.8395	213	219.8975	225.4377	-1.49E-01	-1.98E-01	1	Unchanged Low
Q12891	E08ef5	hyaluronoglucosaminidase 2	331.3833	311	220.4462	287.6363	-5.88E-01	-9.12E-02	1	Unchanged Low
O15162	L08gh1	phospholipid scramblase 1	440.6448	597	220.6688	419.5068	-9.98E-01	4.39E-01	1	Unchanged Low
Q14469	O08ab7	hairy homolog ( <i>Drosophila</i> )	151.2148	251	221.0242	207.739	5.48E-01	7.31E-01	1	Unchanged Low
P06241	P13ab4	FYN oncogene related to SRC; F	108.4214	82.5	221.2951	136.7385	1.06E+00	-3.67E-01	1	Unchanged Low
Q9BVG9	P17gh7	phosphatidylserine synthase 2	225.5812	200	221.5588	215.8454	-2.60E-02	-1.71E-01	1	Unchanged Low
Q9P0P9	K12ef2	hypothetical protein LOC51249	290.4444	434	222.6323	315.5568	-3.84E-01	5.78E-01	1	Unchanged Low
Q9UMF9	L14cd3	eukaryotic translation initiation fa	207.6515	242	222.6344	224.2505	1.01E-01	2.24E-01	1	Unchanged Low
Q03527	L07eb8	proteasome (prosome; macropain)	441.6371	284	222.6794	316.1666	-9.88E-01	4.39E-01	1	Unchanged Low
P31153	J15ab7	methionine adenosyltransferase	245.2111	134	222.7802	200.5541	-1.38E-01	-8.75E-01	1	Unchanged Low
Q04741	D21ef1	empty spratches homolog 1 ( <i>Dros</i> )	240.3769	189	222.7971	217.4148	-1.10E-01	-3.46E-01	1	Unchanged Low
Q13153	L22ef5	p21/Cdc42/Rac1-activated kinase	243.198	277	222.8583	247.6258	-1.26E-01	1.87E-01	1	Unchanged Low
Q9T388	H15ef2	CG1-79 protein	100.7214	181	223.2467	168.2593	1.15E+00	8.44E-01	1	Unchanged Low
Q9HC14	K17gh5	mitochondrial ribosomal protein t	158.7783	200	223.2594	193.9429	4.92E-01	3.31E-01	1	Unchanged Low
P30281	O08ef5	cyclin D3	107.4859	167	223.2751	166.0499	1.05E+00	6.39E-01	1	Unchanged Low
Q9UFI2	P05ef8	DKFZP584K1964 protein	133.0476	210	223.4229	188.8934	7.48E-01	6.60E-01	1	Unchanged Low
Q13011	O23ab4	enoyl Coenzyme A hydratase 1; I	337.9818	273	223.7187	278.2904	-5.95E-01	-3.07E-01	1	Unchanged Low
P09601	E20ef7	heme oxygenase (decycling) 1	166.4519	425	223.7447	278.3661	2.63E-01	1.19E+00	1	Unchanged Low
Q9BVZB	P23gh8	hypothetical protein FLJ14936	126.6889	127	224.0692	159.346	8.23E-01	6.71E-03	1	Unchanged Low
Q13889	A11ab5	general transcription factor IIH; p	112.1935	202	224.1653	179.5227	9.99E-01	8.50E-01	1	Unchanged Low
P49703	P23ab2	ADP-ribosylation factor 4-like	125.6732	91.2	224.1896	147.0234	8.35E-01	-4.62E-01	1	Unchanged Low
Q9GZU7	G11gh4	nuclear LM interactor-interacting	305.5546	150	224.2596	226.5474	-4.46E-01	-1.03E+00	1	Unchanged Low
P10253	M22ab3	glucosidase; alpha; acid (Pompe	187.3998	156	224.2782	189.0733	2.59E-01	-2.69E-01	1	Unchanged Low
Q9Y3V5	B18ef8	hypothetical protein DKFZP586F	303.8477	426	224.4103	318.1897	-4.37E-01	4.89E-01	1	Unchanged Low
O14773	P17ef7	ceroid-lipofuscinosis; neuronal 2;	169.6468	214	224.4535	202.7117	4.04E-01	3.35E-01	1	Unchanged Low
P22061	G13cd1	protein-L-isospartate (D-aspart	118.1783	163	224.5569	168.6387	9.26E-01	4.66E-01	1	Unchanged Low
P14868	K21ab4	aspartyl-tRNA synthetase	117.1946	78.1	225.0996	140.1468	9.42E-01	-5.85E-01	1	Unchanged Low
Q14938	D16ef5	nuclear factor I/X (CCAAT-blnd)	94.58773	84.9	225.3458	134.9545	1.25E+00	-1.55E-01	1	Unchanged Low
Q75968	P21ef3	pannexin 1	215.9189	216	225.5368	219.072	6.29E-02	-1.06E-03	1	Unchanged Low
Q9H1779	C15gh6	hypothetical protein MGC2021	138.4597	313	225.8086	225.7323	7.06E-01	1.18E+00	1	Unchanged Low
Q9BX72	C02gh8	IPF38	168.9682	172	225.8249	188.9468	4.18E-01	2.61E-02	1	Unchanged Low
O43563	G24cd1	solute carrier family 22 (organic c	133.7352	149	225.8428	169.4168	7.56E-01	1.53E-01	1	Unchanged Low
O15142	D17eb2	ARP2 actin-related protein 2 hot	250.3086	215	226.0552	230.3093	-1.47E-01	-2.22E-01	1	Unchanged Low
Q9U411	K17ef4	putative Rab5 GDP/GTP exchange	121.9096	165	226.5205	171.2118	8.94E-01	4.38E-01	1	Unchanged Low
P05231	F21ef7	Interleukin 6 (interferon; beta 2)	240.2349	673	226.5259	379.972	-8.48E-02	1.49E+00	1	Unchanged Low
Q9Y2H0	G24ef8	KIAA0964 protein	279.6086	310	226.545	271.9604	-3.04E-01	1.48E-01	1	Unchanged Low
Q9UJT9	E15cd8	F-box and leucine-rich repeat pr	287.9128	294	226.762	269.5315	-3.44E-01	2.98E-02	1	Unchanged Low
Q9Y308	O23ef1	pelota homolog ( <i>Drosophila</i> )	146.8037	190	226.8083	187.7391	6.28E-01	3.69E-01	1	Unchanged Low
Q9Y6A6	N04ef3	transcription factor (p38 Interactu	174.5425	171	226.9539	190.8287	3.79E-01	-2.97E-02	1	Unchanged Low
Q75300	K18cd2	ribosome binding protein 1 homo	98.67954	73.7	227.0651	133.1515	1.20E+00	4.21E-01	1	Unchanged Low
P51798	L03ef1	chloride channel 7	278.4282	282	228.3119	263.0108	-2.86E-01	1.98E-02	1	Unchanged Low
Q14839	C21ab4	chromodomain helicase DNA bin	104.8847	161	228.3222	164.8091	1.12E+00	6.20E-01	1	Unchanged Low
O60299	O18gh1	KIAA0552 gene product	132.5981	337	228.4246	232.6614	7.85E-01	1.35E+00	1	Unchanged Low
Q9Y6F1	H03ab2	ADP-ribosyltransferase (NAD+; p	248.9844	399	228.5355	292.1577	-1.24E-01	6.80E-01	1	Unchanged Low
O15212	E04ef3	HLA class II region expressed g	250.113	292	228.5829	258.7661	-1.30E-01	2.22E-01	1	Unchanged Low
Q9Y2W2	J14ef2	WW domain binding protein 11	335.0512	304	228.6314	289.1386	-5.51E-01	-1.42E-01	1	Unchanged Low
Q9UKN5	O03cd8	PR domain containing 4	252.6208	80.6	228.6339	187.2825	-1.44E-01	-1.65E+00	1	Unchanged Low
Q90978	C24cd6	Interferon-stimulated transcripto	303.7171	404	228.7768	312.2774	-4.09E-01	4.13E-01	1	Unchanged Low
Q9UHY0	L08ef1	HP1-BP74	295.9512	267	228.8435	263.8122	-3.71E-01	-1.50E-01	1	Unchanged Low
Q9Y248	L13ef2	HSPC037 protein	92.39515	70.3	229.0541	130.5748	1.31E+00	-3.95E-01	1	Unchanged Low
O96019	E21ab2	BAP53	228.9673	345	229.5696	267.9206	3.79E-03	5.92E-01	1	Unchanged Low
P10276	K19ab8	retinol add receptor; alpha	250.0312	122	229.7466	200.7048	-1.22E-01	-1.03E+00	1	Unchanged Low
Q9BUJC7	P22gh8	hypothetical protein MGC4172	136.4413	398	229.8471	254.8265	7.52E-01	1.55E+00	1	Unchanged Low
Q9HAC1	D01gh5	pra1	143.4188	97.5	230.0154	156.9785	6.81E-01	-5.57E-01	1	Unchanged Low
Q93078	M18gh6	H28 histone family; member H	179.9656	203	230.2553	204.3058	3.56E-01	1.72E-01	1	Unchanged Low
P08572	N22ef5	collagen; type IV; alpha 2	70.14126	87.3	230.3868	129.2665	1.72E+00	3.15E-01	1	Unchanged Low
P15056	G10ef5	v-raf murine sarcoma viral oncog	194.1803	174	231.0687	199.7155	2.51E-01	-1.59E-01	1	Unchanged Low
Q15543	J15cd2	TAF13 RNA polymerase II; TATA	222.3129	262	231.2695	238.5733	5.70E-02	2.38E-01	1	Unchanged Low
O14901	J05cd3	TGFβ Inducible early growth resi	277.9069	277	231.5621	262.1749	-2.63E-01	-4.43E-03	1	Unchanged Low
N10gh8	diphosphate dimethylallyl diphos	313.8915	257	231.841	267.6704	-4.37E-01	-2.87E-01	1	Unchanged Low	
P51965	O13cd3	neogenin homolog 1 (chicken)	153.0455	249	232.6926	211.5326	6.04E-01	7.01E-01	1	Unchanged Low
Q9Y3R2	G04cd8	ubiquitin-conjugating enzyme E2	254.2693	93.2	232.9973	216.5887	-4.74E-01	-1.80E+00	1	Unchanged Low
Q94829	G10gh1	importin 13	160.8646	283	233.0208	244.6261	-2.83E-02	1.47E-01	1	Unchanged Low
Q92859	M13ab8	importin 13	160.8646	247	232.3109	213.3188	5.30E-01	6.17E-01	1	Unchanged Low
Q12846	O02cd2	syntaxin 4A (placental)	323.5547	249	232.6926	211.5326	6.04E-01	7.01E-01	1	Unchanged Low
P01286	G15ef1	growth hormone releasing hornc	237.6384	263	233.0208	244.6261	-2.83E-02	1.47E-01	1	Unchanged Low
Q9UH92	L01cd8	transcription factor-like 4	172.7135	195	233.1639	200.1328	4.33E-01	1.72E-01	1	Unchanged Low
O75323	P09ab5	glioblastoma amplified sequence	178.3893	168	233.5843	193.2783	3.89E-01	-8.76E-02	1	Unchanged Low
Q9UCQ33	P07ef2	microtubule-associated protein; f	101.7866	134	234.2195	156.5563	1.20E+00	3.93E-01	1	Unchanged Low
Q9Y3A7	A17ef2	CG-101 protein	402.1639	210	234.3057	282.2981	-7.79E-01	-9.34E-01	1	Unchanged Low
Q9Y2Z0	A17cd7	suppressor of G2 allele of SKP1;	184.6693	256	234.3223	224.9862	3.44E-01	4.71E-01	1	Unchanged Low
P56211	F16ab2	cyclic AMP phosphoprotein; 19 k	276.9734	386	234.3401	299.2676	-2.41E-01	4.81E-01	1	Unchanged Low
P21127	O13ef1	cell division cycle 2-like 2	159.1108	304	234.454	232.4012	5.59E-01	9.32E-01	1	Unchanged Low
Q07866	B23ab7	kinesin 2 (60-70kD)	254.5932	408	234.5156	299.1796	-1.19E-01	6.82E-01	1	Unchanged Low

Q9BT13	H11ef8	KIAA1068 protein	228.7025	230	234.5211	231.0835	3.82E-02	8.33E-03	1	Unchanged Low
Q9H2J4	E11gh6	hypothetical protein MGC3062	238.7573	256	235.0353	243.2412	-2.27E-02	1.00E-01	1	Unchanged Low
Q9NXE5	E10gh2	hypothetical protein FLJ20296	183.8379	399	235.1458	275.9024	2.79E-01	1.04E+00	1	Unchanged Low
Q92572	E17ab4	adaptor-related protein complex	86.23952	209	235.2813	176.703	1.45E+00	1.27E+00	1	Unchanged Low
Q9NXTB	K05gh2	FtsJ homolog 3 (E. coli)	254.7485	277	235.4028	255.685	-1.14E-01	1.20E-01	1	Unchanged Low
O15321	F05cd6	transmembrane 9 superfamily me	295.1129	227	235.695	252.5647	-3.24E-01	-3.79E-01	1	Unchanged Low
O15383	F07cd6	HIV-1 Tat interactive protein 2; 3	402.6554	444	235.7849	360.7235	-7.73E-01	1.39E-01	1	Unchanged Low
O60403	B06cd8	olfactory receptor; family 10; sub	237.7465	282	235.906	245.2774	-1.12E-02	1.41E-01	1	Unchanged Low
P49354	K24ab4	farnesylytransferase; CAAAX box; ε	173.9344	193	235.9155	201.1077	4.40E-01	1.54E-01	1	Unchanged Low
P48039	B07ef6	melatonin receptor 1A	305.0287	208	236.1249	249.7986	-3.69E-01	-5.51E-01	1	Unchanged Low
O43582	C08ab8	solute carrier family 22 (organic c	115.4101	125	236.1587	158.9844	1.03E+00	1.20E+01	1	Unchanged Low
Q9HC89	N24ef10	calpain 10	212.0138	242	236.247	230.2337	1.56E-01	1.93E-01	1	Unchanged Low
P00790	M13ef1	pepsinogen 5; group I (pepsinog	256.009	266	236.6918	253.0491	-1.13E-01	5.77E-02	1	Unchanged Low
Q9NVP1	G01cd6	DEAD/H (Asp-Glu-Ala-Asp/His) t	78.40555	89	236.7778	134.724	1.59E+00	1.83E-01	1	Unchanged Low
Q9UBN1	F23ef3	calcium channel; voltage-depend	269.9719	360	237.0557	289.0967	-1.68E-01	4.16E-01	1	Unchanged Low
P35659	M22cd3	DEK oncogene (DNA binding)	80.02159	77.8	237.1934	131.8712	1.57E+00	-4.06E-02	1	Unchanged Low
P54252	N09ef6	Machado-Joseph disease (spinoc	156.7549	274	237.2775	222.5126	5.98E-01	8.03E-01	1	Unchanged Low
Q14152	L12cd3	eukaryotic translation initiation fa	384.5131	268	237.302	289.8959	-6.19E-01	-4.43E-01	1	Unchanged Low
Q9Y314	E16ef2	ENOS Interacting protein	123.3313	219	237.3058	193.3594	9.44E-01	8.31E-01	1	Unchanged Low
Q9NRCT	E23ef3	sttuln silent mating type Informal	136.0486	328	237.5194	233.7238	8.04E-01	1.27E+00	1	Unchanged Low
P02533	N02ef6	keratin 14 (epidermolytic bullous	203.4102	190	237.6591	210.4458	2.25E-01	-9.66E-02	1	Unchanged Low
O60907	J19cd2	transducin (beta)-like 1 X-linked	175.9553	171	237.7395	194.8701	4.34E-01	-4.19E-02	1	Unchanged Low
P43155	B16ab3	carnitine acetyltransferase	268.355	190	237.8908	238.6829	-2.78E-01	-6.03E-01	1	Unchanged Low
P15077	H08ab8	pyrimidinergic receptor P2Y; G-p	399.9746	248	238.1475	292.1056	-7.12E-01	-6.52E-01	1	Unchanged Low
Q12840	I06ab7	kinesin family member 5A	238.3605	282	238.2407	252.8959	-7.25E-04	2.43E-01	1	Unchanged Low
P26599	A05cd3	polypryimidine tract binding prote	160.4912	345	238.4	247.8557	5.71E-01	1.10E+00	1	Unchanged Low
Q9Y316	M11ef2	C21orf19-like protein	450.6398	327	238.5981	338.8101	-9.17E-01	-4.62E-01	1	Unchanged Low
P24394	O18ab6	Interleukin 4 receptor	309.5199	330	238.6201	292.7071	-3.75E-01	9.24E-02	1	Unchanged Low
P32418	J22gh1	solute carrier family 8 (sodium/ca	171.4935	134	238.7225	181.3894	4.77E-01	-3.56E-01	1	Unchanged Low
P42694	N01ef3	helicase with zinc finger domain	165.7017	146	238.7561	183.6122	5.27E-01	-1.79E-01	1	Unchanged Low
O60755	L09cd3	galanin receptor 3	162.6185	268	238.7669	223.2358	5.54E-01	7.22E-01	1	Unchanged Low
Q16204	A18cd4	DNA segment; single copy; prob:	192.0586	225	238.8166	218.6477	3.14E-01	2.29E-01	1	Unchanged Low
Q12980	N15cd7	Conserved gene telomeric to alp	183.7714	174	238.9231	198.8702	3.79E-01	-7.95E-02	1	Unchanged Low
P08559	N16ab7	pyruvate dehydrogenase (lipoa	375.1479	206	239.4879	273.612	-6.48E-01	-8.63E-01	1	Unchanged Low
Q9Y2L9	K02ef3	host cell factor homolog	127.5142	154	239.6223	173.6438	9.10E-01	2.70E-01	1	Unchanged Low
Q9Y2T2	P17cd7	adaptor-related protein complex	336.9686	395	239.6299	323.8714	-4.92E-01	2.29E-01	1	Unchanged Low
Q13105	K10cd3	zinc finger protein 151 (pH-67)	177.9188	243	240.018	220.1539	4.32E-01	4.47E-01	1	Unchanged Low
Q9H1J1	J12gh5	similar to yeast Upf3; variant A	154.12	183	241.0316	192.8261	6.45E-01	2.50E-01	1	Unchanged Low
Q08756	E01cd1	peptidylprolyl isomerase D (cyc	446.371	203	241.0389	296.8872	-8.89E-01	-1.13E+00	1	Unchanged Low
P38159	F14ab7	RNA binding motif protein; X chr	342.4693	176	241.0429	253.2584	-5.07E-01	-9.58E-01	1	Unchanged Low
Q9Y337	A12cd8	kallikrein 5	215.5515	312	241.2144	256.4089	1.62E-01	5.36E-01	1	Unchanged Low
P25445	A02ef6	tumor necrosis factor receptor su	102.3524	215	241.2257	186.0304	1.24E+01	1.07E+00	1	Unchanged Low
Q9BZH1	P02gh5	membrane-spanning 4-domains;	350.8825	212	241.5154	268.2725	-5.39E-01	-7.24E-01	1	Unchanged Low
O43633	O12ef4	putative breast adenocarcinoma	308.4601	232	241.573	260.7188	-3.53E-01	-4.10E-01	1	Unchanged Low
Q99536	B03cd6	vesicle amine transport protein 1	222.8504	400	241.6698	288.1584	1.17E-01	8.44E-01	1	Unchanged Low
P24557	N11cd1	thromboxane A synthase 1 (plate	326.4482	238	241.6941	268.1689	-4.34E-01	-4.66E-01	1	Unchanged Low
O75369	G16ab4	filamin B; beta (actin binding pro	331.8975	459	241.7672	344.1714	-4.56E-01	4.69E-01	1	Unchanged Low
P50453	H10ab8	serine (or cysteine) proteinase	439.8605	370	242.4005	350.7941	-8.60E-01	-2.49E-01	1	Unchanged Low
P35680	O18cd1	transcription factor 2; hepatic; LF	235.5021	174	242.5943	217.2497	4.28E-02	-4.40E-01	1	Unchanged Low
Q03924	I01gh7	zinc finger protein 117 (HPF9)	257.8571	301	242.7729	267.2646	-8.70E-02	2.24E-01	1	Unchanged Low
Q9NRQ5	F17gh4	FNS protein	361.924	325	242.8257	309.8867	-5.76E-01	-1.56E-01	1	Unchanged Low
Q99867	G12gh7	tubulin; beta polypeptide 4; mem	376.7361	247	243.6773	289.1694	-6.29E-01	-6.08E-01	1	Unchanged Low
Q9H682	B19gh7	A20-binding inhibitor of NF-κB	205.6095	365	243.7949	271.5091	2.46E-01	8.28E-01	1	Unchanged Low
O00148	N12cd5	DEAD/H (Asp-Glu-Ala-Asp/His) t	259.196	140	244.0023	214.3036	-8.71E-02	-6.92E-01	1	Unchanged Low
F11cd8	TCF3 (E2A) fusion partner (In ch	170.7519	295	244.0153	238.7141	5.15E-01	7.91E-01	1	Unchanged Low	
Q9UG51	N05ef3	anaphase-promoting complex su	274.4079	331	244.0324	283.0875	-1.69E-01	2.70E-01	1	Unchanged Low
Q75175	F12cd8	CCR4-NOT transcription compre	230.1579	253	244.0384	242.329	8.45E-02	1.35E-01	1	Unchanged Low
Q9GZQ8	C05gh2	microtubule-associated proteins	261.5987	395	244.0725	300.1702	-1.00E-01	5.94E-01	1	Unchanged Low
P19438	A04ef6	tumor necrosis factor receptor su	233.3188	197	244.3384	224.9565	6.66E-02	-2.43E-01	1	Unchanged Low
Q9NRB8	O04gh4	small protein effector 1 of Cdc42	338.2133	329	244.5729	303.9389	-4.68E-01	-3.97E-02	1	Unchanged Low
Q95162	N10ef8	peroxisomal short-chain alcohol o	154.9486	108	244.9155	169.1352	6.60E-01	-5.27E-01	1	Unchanged Low
Q95279	J22cd3	potassium channel; subfamily K	274.3417	127	244.9972	215.5542	-1.63E-01	-1.11E+00	1	Unchanged Low
Q9NTW4	N21ef8	DKFPZP564A2416 protein	403.4188	219	245.1953	289.1446	-7.18E-01	-8.83E-01	1	Unchanged Low
Q9NW9	H21gh2	hypothetical protein FLJ20730	121.538	207	245.69	191.4607	1.02E+00	7.69E-01	1	Unchanged Low
P40121	P23ab5	capping protein (actin filament);	452.2008	414	245.8846	370.7982	-8.79E-01	-1.26E-01	1	Unchanged Low
Q92456	I04ab3	damage-specific DNA binding pr	99.17314	220	246.0478	188.2339	1.31E+00	1.15E+00	1	Unchanged Low
O43365	K05gh7	homeo box A3	132.7369	196	246.2071	191.5647	8.91E-01	5.60E-01	1	Unchanged Low
Q9NVJ7	O02gh3	DEAD/H (Asp-Glu-Ala-Asp/His) t	336.1927	284	246.3831	288.7892	-4.48E-01	-2.44E-01	1	Unchanged Low
Q9NVY5	H08ef7	serologically defined colon cance	182.4596	178	246.7633	202.4155	4.36E-01	-3.55E-02	1	Unchanged Low
Q9BY40	G12gh8	CDA11 protein	141.0763	131	246.8975	173.0132	8.07E-01	-1.05E-01	1	Unchanged Low
Q9NZ2	O06ef2	hypothetical protein LOC51321	76.41026	135	247.0025	152.875	1.69E+00	8.23E-01	1	Unchanged Low
P29275	K11ab2	adenosine A2b receptor	354.5115	191	247.0615	264.0659	-5.21E-01	-8.95E-01	1	Unchanged Low
Q9NZ0	P22ef1	WW domain-containing adapter	82.72809	71.1	247.6094	133.8158	1.58E+00	-2.18E-01	1	Unchanged Low
Q03111	N03ab7	myeloid/lymphoid or mixed-lineag	225.1377	162	247.8275	211.7891	1.39E-01	-4.71E-01	1	Unchanged Low
Q08499	G21ef6	phosphodiesterase 4D; cAMP-sp	125.5177	92.9	248.1727	155.5405	9.83E-01	-4.34E-01	1	Unchanged Low
Q15628	A20ef8	TNFRSF1A-associated via death	214.1641	250	248.2613	237.3623	2.13E-01	2.21E-01	1	Unchanged Low
Q9Y657	C07cd7	spindlin	217.9487	202	248.4185	222.9201	1.89E-01	-1.07E-01	1	Unchanged Low
Q9UHQ1	I09cd8	nuclear prelamin A recognition fa	312.9614	303	248.5926	288.0624	-3.32E-01	-4.84E-02	1	Unchanged Low
P17980	H24ef6	proteasome (prosome; macropal	331.1488	183	248.6266	257.498	-4.13E-01	-7.81E-01	1	Unchanged Low
P45877	I19ab8	peptidylprolyl isomerase C (cycl	165.0716	169	248.9851	194.3167	5.93E-01	3.30E-02	1	Unchanged Low
O95340	A23cd5	3'-phosphadenosine 5'-phosph	110.9876	88.6	249.0622	149.5355	1.17E+00	-3.26E-01	1	Unchanged Low
Q9H927	F18gh5	hypothetical protein FLJ12448	158.5794	279	249.1478	228.8009	8.52E-01	8.13E-01	1	Unchanged Low
O15172	E11cd4	phosphoserine phosphatase-like	321.9068	291	249.3629	287.4495	-3.68E-01	-1.45E-01	1	Unchanged Low
P01298	F05ab8	pancreatic polypeptide	544.0034	194	249.376	329.1527	-1.13E+00	-1.49E+00	1	Unchanged Low
Q13395	J17cd2	TAR (HIV) RNA binding protein 1	260.7056	234	249.3777	248.0711	-6.41E-02	-1.55E-01	1	Unchanged Low
O15551	G23ab4	claudin 3	279.9519	250	249.4618	259.744	-1.86E-01	-1.64E-01	1	Unchanged Low

P55060	G20ef6	CSE1 chromosome segregation 1	322.1588	276	249.5903	282.6907	-3.68E-01	-2.21E-01	1 Unchanged Low
O43266	E13ab3	UDP-Gal:betaGlcNAc beta 1:4- $\alpha$	316.581	468	249.8072	344.9578	-3.42E-01	5.65E-01	1 Unchanged Low
P04424	J10ab2	argininosuccinate lyase	594.9833	269	250.046	371.2795	-1.25E+00	-1.15E+00	1 Unchanged Low
Q9NWRS	C10gh3	hypothetical protein FLJ20657	171.9643	252	250.1961	224.8496	5.41E-01	5.50E-01	1 Unchanged Low
Q9BUN8	M21gh8	hypothetical protein MGC3067	165.6904	175	250.2847	197.0059	5.95E-01	7.92E-02	1 Unchanged Low
P49760	G01ab4	CDC-like kinase 2	69.23701	97.1	250.3266	138.8925	1.85E+00	4.88E-01	1 Unchanged Low
Q8UEG3	E01gh7	myotubularin related protein 3	367.623	236	250.553	284.5589	-5.53E-01	-6.42E-01	1 Unchanged Low
Q9PDY6	N07ef1	chromosome 3 open reading frar	268.1158	256	250.6098	258.2636	-9.74E-02	-6.63E-02	1 Unchanged Low
Q92535	M06ab8	phosphatidylinositol glycan; class	218.2502	172	250.9192	213.6071	2.01E-01	-3.46E-01	1 Unchanged Low
Q00577	A24gh7	purine-rich element binding prot	839.6	273	251.0214	454.6488	-1.74E+00	-1.62E+00	1 Unchanged Low
O75717	L21ab2	AND-1 protein	225.9974	250	251.1522	242.2724	1.52E-01	1.44E-01	1 Unchanged Low
P04278	L09cd1	sex hormone-binding globulin	215.6067	196	251.1944	221.0173	2.20E-01	-1.36E-01	1 Unchanged Low
P51124	G19ab5	granzyme M (lymphocyte met-as)	108.9072	114	251.2498	158.1827	1.21E+00	7.09E-02	1 Unchanged Low
P15259	P04eb7	phosphoglycerate mutase 2 (mus)	333.2442	363	251.6608	315.8301	-4.05E-01	1.22E-01	1 Unchanged Low
Q12893	O13cd7	PL6 protein	174.3077	280	252.0241	235.3565	5.32E-01	6.82E-01	1 Unchanged Low
P57738	A11gh2	T-cell leukemia translocation site	166.5683	232	252.2165	217.0429	5.99E-01	4.80E-01	1 Unchanged Low
P24863	O22ef5	cyclin C	668.8834	523	252.3823	481.4089	-1.41E-01	-3.55E-01	1 Unchanged Low
Q9Y370	H03ef2	CG160 protein	153.6349	157	252.5038	187.803	7.17E-01	2.82E-02	1 Unchanged Low
Q9HD89	E04gh4	found in inflammatory zone 3	189.8748	182	252.7224	208.2163	4.13E-01	-6.07E-02	1 Unchanged Low
O14807	N04cd7	muscle RAS oncogene homolog	105.1243	181	252.8147	179.5238	1.27E+00	7.81E-01	1 Unchanged Low
Q13435	I07cd7	splicing factor 3b; subunit 2; 145k	270.3354	268	252.8473	263.6077	-9.65E-02	-4.45E-02	1 Unchanged Low
Q9UJMY4	F19cd8	sorting nexin 12	178.8659	227	253.0138	219.6698	5.00E-01	3.45E-01	1 Unchanged Low
Q43929	C04eb8	origin recognition complex; subunit	267.5605	354	253.265	291.5955	-7.92E-02	4.04E-01	1 Unchanged Low
Q98ZQ1	H14gh7	chromosome 1 open reading frar	219.6632	362	253.5183	278.4192	2.07E-01	7.21E-01	1 Unchanged Low
P55042	K03ef5	Ras-related associated with diab	300.5794	514	253.5279	355.8906	-2.46E-01	7.73E-01	1 Unchanged Low
Q92870	K18ef1	amyloid beta (A4) precursor prot	76.07104	77.9	253.5714	135.8422	1.74E+00	3.40E-02	1 Unchanged Low
P33778	C19gh7	H2B histone family; member F	169.4431	391	253.9554	271.5522	5.84E-01	1.21E+00	1 Unchanged Low
Q9UL23	K22cd8	apoptosis-associated speck-like	255.9554	517	254.0856	342.2046	-1.06E-02	1.01E+00	1 Unchanged Low
Q13485	A20ef5	MAD; mothers against decapent	163.1373	181	254.1546	199.4935	6.40E-01	1.51E-01	1 Unchanged Low
Q9H684	C24gh5	zinc finger protein 335	326.6826	261	254.3385	280.5396	-3.61E-01	-3.26E-01	1 Unchanged Low
Q9HF8	O06gh7	hypothetical protein FLJ20958	190.1073	258	254.7196	234.2579	4.22E-01	4.40E-01	1 Unchanged Low
Q92508	B17gh1	KIAA0233 gene product	241.1859	216	255.0491	237.2652	6.80E-02	-1.62E-01	1 Unchanged Low
Q9UM47	C15ab8	Notch homolog 3 ( <i>Drosophila</i> )	64.97745	132	255.0839	150.552	1.97E+00	1.02E+00	1 Unchanged Low
P18084	E17ef7	integrin; beta 5	259.2818	129	255.1335	214.6124	-2.33E-02	-1.00E+00	1 Unchanged Low
Q99462	K22gh6	ubiquitin-conjugating enzyme E2	207.6691	179	255.2632	213.9424	2.98E-01	-2.15E-01	1 Unchanged Low
O75619	J10ef7	RNA helicase-related protein	198.1059	335	255.6713	262.7733	3.68E-01	7.56E-01	1 Unchanged Low
Q92733	K07cd1	papillary renal cell carcinoma (rrz	200.3207	260	256.1407	238.8334	3.55E-01	3.76E-01	1 Unchanged Low
Q15796	H21ab7	MAD; mothers against decapent	376.8422	446	256.2171	359.5423	-5.57E-01	2.42E-01	1 Unchanged Low
P15291	E07ab3	UDP-Gal:betaGlcNAc beta 1:4- $\alpha$	411.9325	403	256.9006	357.1444	-6.81E-01	-3.31E-02	1 Unchanged Low
Q99417	I07cd8	c-myc binding protein	264.1386	256	256.9088	259.037	-4.00E-02	-4.48E-02	1 Unchanged Low
P06732	D09ab4	creatine kinase; muscle	202.527	127	257.2272	195.4365	3.45E-01	-6.78E-01	1 Unchanged Low
P50570	K13ab5	dynamin 2	248.1369	228	257.2474	244.4335	5.20E-02	-1.23E-01	1 Unchanged Low
Q9V5A9	F20ef2	high-glucose-regulated protein 8	359.385	371	257.3917	329.2557	-4.82E-01	4.59E-02	1 Unchanged Low
Q92841	B17cd6	DEAD/H (Asp-Glu-Ala-Asp/His) t	229.8916	270	257.9255	252.4572	1.66E-01	2.30E-01	1 Unchanged Low
P1808	B22cd2	t-complex-associated-testis-exprn	182.2992	245	257.9487	228.2619	5.01E-01	4.24E-01	1 Unchanged Low
D95758	H23cd5	R0D1 regulator of differentiation	411.9888	462	258.1758	377.5392	-6.74E-01	1.67E-01	1 Unchanged Low
P32970	I15ef5	tumor necrosis factor (lgand) su	443.4158	456	258.4229	386.0177	-7.79E-01	4.11E-02	1 Unchanged Low
O75689	K21cd7	cerataurin; alpha 1	191.7263	327	258.6352	259.1653	4.32E-01	7.71E-01	1 Unchanged Low
P55072	O06cd4	valosin-containing protein	466.7034	363	258.8411	362.8018	-8.50E-01	-3.63E-01	1 Unchanged Low
P47813	A16ab4	eukaryotic translation initiation fa	486.6493	337	259.0481	360.7943	-9.10E-01	-5.31E-01	1 Unchanged Low
Q15532	J03cd2	synovial sarcoma translocation; c	190.8535	212	259.1488	220.5805	4.41E-01	1.50E-01	1 Unchanged Low
Q15813	M19cd2	tubulin-specific chaperone e	151.2337	166	259.2747	192.1296	7.78E-01	1.33E-01	1 Unchanged Low
P14373	B08cd2	ret finger protein	282.5757	270	259.3599	270.5765	-1.24E-01	-6.68E-02	1 Unchanged Low
O14980	G02cd3	exportin 1 (CRM1 homolog; yeas	239.4965	207	259.7187	235.5264	1.17E-01	-2.08E-01	1 Unchanged Low
P07942	P20ef6	laminin; beta 1	71.03574	92.4	259.7579	141.0764	1.87E-00	3.80E-01	1 Unchanged Low
P53041	C20cd1	protein phospholase 5; catalytic	272.5094	196	259.8136	242.7533	-6.88E-02	-4.76E-01	1 Unchanged Low
Q07820	E12ef6	myeloid cell leukemia sequence	362.5007	243	260.0329	288.4688	-4.79E-01	-5.78E-01	1 Unchanged Low
P53816	E04cd7	HRAS-like suppressor 3	606.0957	558	260.1655	474.8201	-1.22E+00	-1.19E-01	1 Unchanged Low
Q9P1C8	E05gh4	hypothetical protein PRO2577	238.9909	205	260.3147	234.8631	1.23E-01	-2.19E-01	1 Unchanged Low
P51966	O21cd3	ubiquitin-conjugating enzyme E2	148.3528	243	260.3185	217.1092	8.11E-01	7.10E-01	1 Unchanged Low
Q99739	M03cd7	plm-2 oncogene	178.694	274	260.4482	237.5556	5.44E-01	6.14E-01	1 Unchanged Low
P35913	N14ab7	phosphodiesterase 6B; cGMP-sp	199.3654	173	260.5708	210.8879	3.86E-01	-2.07E-01	1 Unchanged Low
P52756	J24cd5	RNA binding motif protein 5	280.6537	230	261.0637	257.2441	-1.04E-01	-2.87E-01	1 Unchanged Low
Q9N0K5	K17gh3	hypothetical protein FLJ20004	130.163	197	261.2642	196.0576	1.01E+00	5.96E-01	1 Unchanged Low
Q14498	O06cd5	RNA-binding region (RNP1; RR&	196.0463	216	261.5829	224.4664	4.16E-01	1.38E-01	1 Unchanged Low
P28069	A03ab8	POU domain; class 1; transcriptk	261.1822	206	261.7762	243.064	3.28E-03	-3.41E-01	1 Unchanged Low
P51397	E20ab5	death-associated protein	348.1009	312	261.9342	307.4499	-4.10E-01	-1.57E-01	1 Unchanged Low
Q9NU18	C24gh7	putative methyltransferase	157.3551	329	262.0287	249.4637	7.36E-01	1.06E+00	1 Unchanged Low
O00322	M09cd7	urokinin 1A	223.5266	295	262.0282	260.1175	2.30E-01	3.99E-01	1 Unchanged Low
P78368	I09ab4	casein kinase 1; gamma 2	211.1048	272	262.1137	248.257	3.12E-01	3.63E-01	1 Unchanged Low
Q01081	I22cd4	U2(RNU2) small nuclear RNA au	138.1533	91.3	262.1811	163.878	9.24E-01	-5.98E-01	1 Unchanged Low
Q43193	J15ab5	G protein-coupled receptor 38	69.57316	206	262.3031	179.1305	1.91E+00	1.56E+00	1 Unchanged Low
Q9Y3B0	M03ef2	CG1-105 protein	174.5026	177	262.5458	204.6742	5.89E-01	2.03E-02	1 Unchanged Low
Q9NV80	H05gh3	WD repeat domain 12	178.5139	279	262.6286	239.9609	5.57E-01	6.43E-01	1 Unchanged Low
Q9Y473	O18cd4	zinc finger protein 175	141.3794	275	263.1093	226.3406	8.96E-01	9.57E-01	1 Unchanged Low
Q9Y548	L20gh2	hypothetical protein DJ167A19.1	233.5442	240	263.4412	245.7773	1.74E-01	4.14E-02	1 Unchanged Low
Q13952	N15ef6	nuclear transcription factor Y; ga	241.7469	354	263.6055	286.4173	1.25E-01	5.50E-01	1 Unchanged Low
P18615	K17cd3	RD RNA-binding protein	237.0199	242	263.7642	247.7362	1.54E-01	3.25E-02	1 Unchanged Low
P33241	B23ef1	lymphocyte-specific protein 1	94.80267	131	264.2422	163.4955	1.48E+00	4.71E-01	1 Unchanged Low
O15116	C01ef4	Lsm1 protein	344.8146	479	264.6979	362.8572	-3.81E-01	4.74E-01	1 Unchanged Low
P50897	A11ab8	palmitoyl-protein thioesterase 1 (	126.6311	142	264.8236	177.9418	1.06E+00	1.69E-01	1 Unchanged Low
	F20gh8	MADP-1 protein	134.6124	228	264.9564	209.3298	9.77E-01	7.63E-01	1 Unchanged Low
Q9Y3A5	G12ef2	CG1-97 protein	469.4567	544	265.0744	426.2946	-8.25E-01	2.14E-01	1 Unchanged Low
Q9BV71	G03gh6	leukocyte receptor cluster (LRC)	282.5457	328	265.5443	291.9599	-8.95E-02	2.14E-01	1 Unchanged Low
Q9UM44	E10cd7	HERV-H LTR-associating 2	180.7238	119	265.5625	188.5666	5.55E-01	-5.98E-01	1 Unchanged Low
Q9UGC7	A05gh3	similar to prokaryotic-type class I	289.9756	362	265.7778	306.0797	-1.26E-01	3.22E-01	1 Unchanged Low

P49146	G01ab8	neuropeptide Y receptor Y2	222.0084	57.8	265.9266	181.9126	2.60E-01	-1.94E+00	1	Unchanged Low
P54687	I03ab3	branched chain aminotransferase	103.4218	93.8	266.0547	154.4299	1.36E+00	-1.41E-01	1	Unchanged Low
O60884	O09cd6	DnaJ (Hsp40) homolog; subunit I	330.3137	367	266.0819	321.0577	-3.12E-01	1.51E-01	1	Unchanged Low
Q9NVC6	J01cd7	cofactor required for Sp1 transcript	183.0562	150	266.1556	199.8392	5.40E-01	-2.84E-01	1	Unchanged Low
O43399	G06cd2	tumor protein D52-like 2	283.4636	348	266.2168	299.1558	-9.06E-02	2.95E-01	1	Unchanged Low
O75880	K22cd2	SCO cytochrome c oxidase defecte	156.7184	117	266.2419	179.8238	7.85E-01	-4.28E-01	1	Unchanged Low
P49406	F01gh1	mitochondrial ribosomal protein I	577.0339	352	266.3918	398.6973	-1.12E+00	-7.10E-01	1	Unchanged Low
Q9NYK5	E15gh2	mitochondrial ribosomal protein I	473.2712	449	266.7642	396.3322	-8.27E-01	-7.81E-02	1	Unchanged Low
O15428	P16cd2	protein (peptidyl-prolyl cis/trans I	185.1313	249	267.1449	233.6377	5.29E-01	4.25E-01	1	Unchanged Low
O14842	K04ab5	G protein-coupled receptor 40	222.6002	170	267.4241	219.8563	2.65E-01	-3.93E-01	1	Unchanged Low
O15262	I06cd6	ring finger protein 3	243.845	401	267.4275	304.1323	1.33E-01	7.18E-01	1	Unchanged Low
Q9NP61	J01ef3	ADP-ribosylation factor GTPase	344.6989	175	267.443	262.4544	-3.66E-01	-9.76E-01	1	Unchanged Low
O15491	P22cd5	WD-repeat protein	254.8166	355	267.6951	292.4461	7.23E-02	4.80E-01	1	Unchanged Low
O75390	P01ab5	citrate synthase	656.561	312	268.0488	412.1526	-1.29E+00	-1.07E+00	1	Unchanged Low
P57088	I12gh3	hypothetical protein FLJ10525	377.5067	349	268.1833	331.588	-4.93E-01	-1.13E-01	1	Unchanged Low
Q9NRY6	K06gh4	phospholipid scramblase 3	272.0774	334	268.2248	291.4542	-2.06E-02	2.96E-01	1	Unchanged Low
O15403	E05cd5	solute carrier family 16 (monocar	384.2992	73.5	268.3423	242.0422	-5.18E-01	-2.39E+00	1	Unchanged Low
Q9BPZ5	K09gh6	hypothetical protein MGC9123	127.3745	286	268.7928	227.363	1.08E+00	1.17E+00	1	Unchanged Low
P10301	P01cd2	related RAS viral (v-ras) oncogene	314.4978	204	268.8367	262.4726	-2.26E-01	-6.24E-01	1	Unchanged Low
A20gh7	HLA-B associated transcript 4	168.0802	234	269.0656	223.8166	6.79E-01	4.79E-01	1	Unchanged Low	
Q9P018	A08ef8	HS4C142 protein	196.1899	346	269.5447	270.6564	4.58E-01	8.20E-01	1	Unchanged Low
Q9Y4H2	L10cd3	Insulin receptor substrate 2	297.029	329	270.4962	298.8227	-1.35E-01	1.47E-01	1	Unchanged Low
Q9UJX3	F04ef2	anaphase-promoting complex sub	210.2906	204	270.642	228.4449	3.64E-01	-4.10E-02	1	Unchanged Low
Q9H5X0	O01gh6	hypothetical protein MGC2941	333.5834	308	270.759	304.1289	-3.01E-01	-1.15E-01	1	Unchanged Low
Q92820	H23cd4	gamma-glutamyl hydrolase (con)	78.13783	101	271.925	150.359	1.80E+00	3.70E-01	1	Unchanged Low
Q9UKH3	K15ab2	ADP-ribosyltransferase (NAD <sup>+</sup> )	337.297	450	271.9944	352.9975	-3.10E-01	4.15E-01	1	Unchanged Low
Q9NW8C	N13gh2	hypothetical protein FLJ10120	315.7654	301	272.0013	296.1206	-2.15E-01	-7.10E-02	1	Unchanged Low
O14965	I07cd2	serine/threonine kinase 6	139.2727	101	272.158	170.6789	9.67E-01	-4.69E-01	1	Unchanged Low
P50613	B11ef5	cyclin-dependent kinase 7 (MO1)	286.8535	423	272.2018	327.4234	-7.56E-01	5.61E-01	1	Unchanged Low
Q9H1C4	H08gh7	unc-93 homolog B1 (C. elegans)	348.8713	501	272.3385	374.1085	-3.57E-01	5.22E-01	1	Unchanged Low
P21851	E13ab4	adaptor-related protein complex	338.7753	373	272.4617	328.1045	3.14E-01	1.39E-01	1	Unchanged Low
Q9UGJ0	B14ef2	protein kinase; AMP-activated; gr	425.3015	543	272.5312	413.4782	-6.42E-01	3.51E-01	1	Unchanged Low
P04035	D17ab6	3-hydroxy-3-methylglutaryl-Coen	242.9132	169	273.2324	228.5315	1.70E-01	-5.20E-01	1	Unchanged Low
Q9UKY7	K03gh3	hypothetical protein H41	643.0085	272	273.736	396.2551	-1.23E+00	-1.24E+00	1	Unchanged Low
O95478	B18gh1	hypothetical protein YR-29	248.2059	221	273.8047	247.5607	1.42E-01	-1.70E-01	1	Unchanged Low
Q9Y3W9	B16ef8	steirin/SUMO-specific protease	220.4064	333	274.1753	275.7562	3.15E-01	5.94E-01	1	Unchanged Low
Q9V325	A20ef2	CGI-36 protein	346.618	338	274.2434	319.4542	-3.38E-01	-3.85E-02	1	Unchanged Low
Q92854	B09cd6	sema domain; Immunoglobulin d	342.6474	183	274.4146	266.8232	-3.20E-01	-9.02E-01	1	Unchanged Low
P16106	O08gh6	H3 histone family; member C	105.4744	221	274.8424	200.5879	1.38E+00	1.07E+00	1	Unchanged Low
O43143	M05ab4	DEAD/H (Asp-Glu-Ala-Asp/His) t	412.7015	349	274.9731	345.6042	-5.86E-01	-2.41E-01	1	Unchanged Low
Q13547	L12ef6	histone deacetylase 1	375.5725	372	275.2293	340.9663	-4.48E-01	-1.34E-02	1	Unchanged Low
Q9HF9	D11gh5	hypothetical protein FLJ22313	306.5811	290	275.269	290.6336	-1.55E-01	-8.00E-02	1	Unchanged Low
Q9NX18	M08gh2	hypothetical protein FLJ20487	311.71	394	275.6418	327.1007	-1.77E-01	3.38E-01	1	Unchanged Low
O94764	P03cd5	RAN binding protein 9	256.3223	268	275.8144	266.5947	1.06E-01	6.24E-02	1	Unchanged Low
P82909	N18gh8	mitochondrial ribosomal protein L	261.4618	343	275.8463	293.6016	7.73E-02	3.94E-01	1	Unchanged Low
Q9UI07	D18ef8	likely ortholog of mouse heat shc	199.8914	199	276.061	225.0966	4.66E-01	-4.00E-03	1	Unchanged Low
P20337	M01ef5	RAB3B; member RAS oncogene	214.8304	126	276.148	205.8132	3.62E-01	-7.65E-01	1	Unchanged Low
Q07960	B22ab2	Rho GTPase activating protein 1	219.98	218	276.1684	237.9303	3.28E-01	-1.55E-02	1	Unchanged Low
P49448	P03cd7	Glutamate dehydrogenase-2	344.3683	229	276.2751	283.2713	-3.16E-01	-5.88E-01	1	Unchanged Low
Q9NX48	K08gh2	hypothetical protein FLJ20442	493.7568	601	276.8343	457.1855	-8.35E-01	2.83E-01	1	Unchanged Low
Q9NV56	J03gh3	chromosome 20 open reading frz	138.9543	104	277.4945	173.6478	9.98E-01	-4.11E-01	1	Unchanged Low
O00154	L21cd7	brain acyl-CoA hydrolase	173.5669	189	277.5737	213.4547	6.77E-01	1.25E-01	1	Unchanged Low
Q9UI70	B04ef1	nucleolar protein ANK1	307.7657	349	277.6076	311.4328	-1.49E-01	1.81E-01	1	Unchanged Low
P26045	N17ab5	protein tyrosine phosphatase; no	412.2292	315	277.6603	334.8518	-5.70E-01	-3.90E-01	1	Unchanged Low
Q9Y2A8	C24ef3	CD209 antigen-like	72.2122	91.3	277.8103	147.0989	1.94E+00	3.38E-01	1	Unchanged Low
Q9BZ89	F08gh7	phospholipase A2; group XII	175.384	216	277.9804	223.0558	6.64E-01	2.99E-01	1	Unchanged Low
P35052	J24ab4	glycan 1	214.4355	173	278.2085	221.7567	3.76E-01	-3.13E-01	1	Unchanged Low
Q9H0S9	K21gh7	nuclear receptor binding factor-2	80.19669	155	278.4321	171.2074	1.80E+00	9.51E-01	1	Unchanged Low
Q15654	I07ef7	thyroid hormone receptor interac	264.295	238	278.8016	260.4802	7.71E-02	-1.49E-01	1	Unchanged Low
P51948	I09ab7	menage a trois 1 (CAK assembly	239.1769	272	278.9368	263.2799	2.22E-01	1.84E-01	1	Unchanged Low
Q13133	B20cd5	nuclear receptor subfamily 1; gro	276.5554	260	279.1408	272.0232	1.34E-02	-8.70E-02	1	Unchanged Low
Q9P0J9	H22gh3	goliath protein	337.3229	215	279.5646	277.1331	-2.71E-01	-6.53E-01	1	Unchanged Low
Q15545	G23db8	monocyte to macrophage differen	136.5038	94	279.6415	170.0401	1.03E+01	-5.39E-01	1	Unchanged Low
P28325	E09ab5	cystatin D	371.8792	309	279.7092	320.2206	-4.10E-01	-2.65E-01	1	Unchanged Low
Q94985	O04ef8	calsyntenin 1	137.0471	205	279.921	207.2587	1.03E+01	5.80E-01	1	Unchanged Low
P48634	M03cd4	HLA-B associated transcript 2	266.8369	179	280.5497	241.9692	7.23E-02	-5.80E-01	1	Unchanged Low
Q9BRL6	O15gh7	Splicing factor; arginine/serine-ri	220.3804	304	280.5881	268.4079	3.48E-01	4.65E-01	1	Unchanged Low
Q94851	E05gh1	KIAA0750 gene product	108.6672	172	280.9738	187.2689	1.37E+00	6.64E-01	1	Unchanged Low
Q9NW56	E20gh3	hypothetical protein FLJ10305	240.4538	314	281.002	278.4551	2.25E-01	3.85E-01	1	Unchanged Low
Q9H6X8	P19gh5	CasL interacting molecule	183.3739	302	281.185	255.4932	6.17E-01	7.19E-01	1	Unchanged Low
P41217	N13ab7	antigen identified by monoclonal	325.1642	166	281.3505	257.5072	-2.09E-01	-9.70E-01	1	Unchanged Low
P31512	P04ab4	flavin containing monooxygenase	192.4074	276	281.6555	249.9252	5.50E-01	5.19E-01	1	Unchanged Low
Q15425	H05cd2	SA hypertension-associated hor	186.2788	151	281.9205	206.4709	5.98E-01	-3.01E-01	1	Unchanged Low
P40306	L05ab8	proteasome (prosome; macropain	408.3043	513	281.9429	400.975	-5.34E-01	3.28E-01	1	Unchanged Low
Q9NW28	O02gh2	hypothetical protein FLJ20514	287.569	146	281.9498	238.3826	-2.85E-02	-9.82E-01	1	Unchanged Low
P57073	E22ef8	SRY (sex determining region Y)-	202.5886	268	281.9705	251.002	4.77E-01	4.06E-01	1	Unchanged Low
Q9Y450	H22cd6	HBS1-like (S. cerevisiae)	230.8266	312	282.4288	274.9973	2.91E-01	4.34E-01	1	Unchanged Low
P04062	O08ab3	glucosidase; beta; acid (includes	295.5318	389	282.6453	322.2918	-6.43E-02	3.95E-01	1	Unchanged Low
O75065	E22gh1	phosphodiesterase 4D interactin	168.0201	154	282.6456	201.6823	7.50E-01	-1.22E-01	1	Unchanged Low
Q9ULX2	F09ef3	NIMA (never in mitosis gene a)-n	288.5578	208	283.1715	259.9871	-2.72E-02	-4.71E-01	1	Unchanged Low
Q99871	C06ef4	three prime repair exonuclease 2	205.6083	225	283.2504	237.9086	4.62E-01	1.29E-01	1	Unchanged Low
Q93065	H15cd6	PERB11 family member in MHC	295.7132	457	283.4269	345.3524	-6.12E-02	6.28E-01	1	Unchanged Low
Q43837	B12ab7	lscitrate dehydrogenase 3 (NAC	348.9961	298	283.6422	310.0846	-2.99E-01	-2.30E-01	1	Unchanged Low
Q9H9L3	L06gh7	hypothetical protein FLJ12671	209.5906	279	283.6912	257.4051	4.37E-01	4.12E-01	1	Unchanged Low
Q13740	A18ab2	activated leucocyte cell adhesion	231.4555	253	283.7582	256.0277	2.94E-01	1.28E-01	1	Unchanged Low
Q12888	L09cd2	tumor protein p53 binding protein	132.9276	223	283.8572	213.3434	1.09E+00	7.48E-01	1	Unchanged Low

P78318	J13eb6	immunoglobulin (CD79A) binding	423.8715	512	283.9511	406.4772	-5.78E-01	2.71E-01	1	Unchanged	Low
P48436	K24cd1	SRY (sex determining region Y)-	345.2087	197	284.0786	275.3736	-2.81E-01	-8.10E-01	1	Unchanged	Low
P16065	B19ef1	insulin-like growth factor binding	286.6516	283	284.2331	284.4952	-1.22E-02	-2.05E-02	1	Unchanged	Low
Q9ULW6	F22cd8	nucleosome assembly protein 14	223.0694	148	284.7117	218.587	3.52E-01	-5.92E-01	1	Unchanged	Low
O95154	N03cd7	aldo-keto reductase family 7; mei	299.8079	298	284.8919	294.419	-7.41E-02	-7.00E-03	1	Unchanged	Low
O95169	P14ab8	NADH dehydrogenase (ubiquinol)	374.2624	199	285.0096	286.0758	-3.93E-01	-9.12E-01	1	Unchanged	Low
Q99982	C24ef4	XIAP associated factor-1	63.10609	116	285.0252	154.8111	2.18E+00	8.82E-01	1	Unchanged	Low
Q99470	F14cd2	stromal cell-derived factor 2	230.3684	316	285.1394	277.1416	3.08E-01	4.56E-01	1	Unchanged	Low
P16104	N19ab5	H2A histone family; member X	234.8351	195	285.2056	238.3532	2.80E-01	-2.68E-01	1	Unchanged	Low
Q9UG25	B04ef8	SOCS box-containing WD protein	213.293	398	285.5592	298.9147	4.21E-01	9.00E-01	1	Unchanged	Low
Q13158	C21cd4	Fas (TNFRSF6)-associated via d	263.0157	281	285.9553	276.784	1.21E-01	9.74E-02	1	Unchanged	Low
Q9NW32	D10gh2	hypothetical protein FLJ10346	235.0532	386	286.3524	302.6214	2.85E-01	7.17E-01	1	Unchanged	Low
O95153	M05cd5	peripheral benzodiazepine receptor	155.1624	231	287.1271	224.5106	8.88E-01	5.75E-01	1	Unchanged	Low
Q9BQ73	H06gh7	hypothetical protein FKSG28	212.0736	297	287.201	265.3817	4.37E-01	4.85E-01	1	Unchanged	Low
Q15426	C02ef7	protein tyrosine phosphatase; ret	296.9619	441	287.2583	341.7927	-4.79E-02	5.71E-01	1	Unchanged	Low
Q92858	L12ab2	atonal homolog 1 (Drosophila)	611.3779	278	287.2641	392.3029	-1.06E+00	-1.14E+00	1	Unchanged	Low
Q16849	P15ab8	protein tyrosine phosphatase; ret	145.9896	556	287.3262	162.9842	9.77E-01	-1.39E+00	1	Unchanged	Low
P11279	D07ab7	lysosomal-associated membrane	369.9925	310	287.3935	322.5735	-3.64E-01	-2.54E-01	1	Unchanged	Low
Q96ii1	I16gh7	hypothetical protein MGCG14961	103.7251	807	287.4071	157.2667	1.47E+00	-3.63E-01	1	Unchanged	Low
P78504	O20ab2	jagged 1 (Alagille syndrome)	255.0945	347	287.4633	296.4108	1.72E-01	4.43E-01	1	Unchanged	Low
O75937	G06ef3	DnaJ (Hsp40) homolog; subfamily	294.9992	264	287.503	282.0586	-3.71E-02	-1.62E-01	1	Unchanged	Low
O60575	O16ef4	serine protease inhibitor; Kazal type	142.2326	152	287.9	194.1988	1.02E+00	1.00E-01	1	Unchanged	Low
Q9NYP7	K05gh5	homolog of yeast long chain poly	299.2029	187	288.1627	257.9759	-5.42E-02	-6.81E-01	1	Unchanged	Low
O95436	H01cd6	solute carrier family 34 (sodium/potassium)	238.6021	425	288.3247	317.3784	2.73E-01	8.34E-01	1	Unchanged	Low
O95324	B15ab2	ATP-binding cassette; sub-family	267.207	275	288.4558	277.0901	1.08E-01	3.94E-02	1	Unchanged	Low
Q9UOFS	B08ef3	ribosomal protein L36	519.2003	425	288.5855	410.9115	-8.47E-01	-2.89E-01	1	Unchanged	Low
P13010	K12ef6	X-ray repair complementing deficiency	174.6996	256	288.9405	239.8403	7.26E-01	5.51E-01	1	Unchanged	Low
Q9UJZ1	P03cd8	stomatin (EPBT2)-like 2	490.6115	272	289.2003	350.5499	-7.63E-01	-8.52E-01	1	Unchanged	Low
P50281	I18ab7	matrix metalloproteinase 14 (merlin)	126.7204	196	289.8803	204.0657	1.19E+00	6.25E-01	1	Unchanged	Low
P15927	B08cd1	replication protein A2 (32kD)	100.0172	194	290.3306	194.7022	1.54E+00	9.54E-01	1	Unchanged	Low
O75496	B02ef1	geminin	466.4376	454	290.7216	403.7854	-6.82E-02	-3.84E-02	1	Unchanged	Low
Q9P1E3	C23gh4	presentin/ins associated rhomboid-	232.5496	263	291.2445	262.3787	3.25E-01	1.79E-01	1	Unchanged	Low
P40189	B14ab6	interleukin 6 signal transducer (gp	330.8834	315	291.3287	312.5572	-1.84E-01	-6.89E-02	1	Unchanged	Low
Q9V259	H03ab4	choline kinase-like	328.1801	375	291.3288	331.5557	-1.72E-01	1.93E-01	1	Unchanged	Low
O00633	C12ef5	phosphatase and tensin homolog	199.7323	189	291.6118	226.7943	5.46E-01	-7.94E-02	1	Unchanged	Low
Q13432	H13cd5	unc-119 homolog (C. elegans)	127.1818	268	291.793	229.0999	1.20E+00	1.08E+00	1	Unchanged	Low
Q9Y677	E03ef2	COP9 constitutive photomorphogenic	186.9367	204	291.9539	227.7917	6.43E-01	1.29E-01	1	Unchanged	Low
Q9BW24	D03ef8	KIAA0576 protein	170.3265	240	292.9836	234.5628	7.83E-01	4.97E-01	1	Unchanged	Low
Q9NSD9	B12cd5	phenylalanyl-tRNA synthetase beta	226.6641	219	293.111	246.1288	3.71E-01	-5.22E-02	1	Unchanged	Low
Q9NWQ0	C16gh3	hypothetical protein FLJ20695	497.4612	656	293.1904	482.3238	-7.63E-01	4.00E-01	1	Unchanged	Low
Q9NWTF6	C02gh3	hypoxia-inducible factor 1; alpha	521.7793	276	293.7543	363.8746	-8.29E-01	-9.18E-01	1	Unchanged	Low
Q9UPN3	J12ef7	microtubule-actin crosslinking fat	578.3578	563	294.1533	478.6344	-9.75E-01	-3.78E-02	1	Unchanged	Low
Q96HW0	A06gh7	zinc finger protein 38 (KOX 25)	126.7599	355	294.3016	258.7634	1.22E+00	1.49E+00	1	Unchanged	Low
Q14257	F18ab8	reticulocalbin 2; EF-hand calcium	237.966	217	295.1469	249.8842	3.11E-01	-1.36E-01	1	Unchanged	Low
Q9NRJS	J05gh4	poly(A) polymerase beta (latsilis)	379.2857	276	295.7341	316.91	-3.59E-01	-4.60E-01	1	Unchanged	Low
P23280	P02ab3	carbonic anhydrase VI	137.6155	102	296.1358	178.6789	1.11E+00	-4.28E-01	1	Unchanged	Low
Q14677	I02gh1	KIAA0171 gene product	330.738	204	296.1674	277.0019	-1.59E-01	-6.96E-01	1	Unchanged	Low
Q9Y394	H17ef2	CGI-86 protein	471.0368	358	296.7589	375.1673	6.67E-01	-3.97E-01	1	Unchanged	Low
Q9UKX5	L18cd7	Integrin; alpha 11	99.18133	126	297.0397	173.978	1.58E-01	-3.42E-01	1	Unchanged	Low
Q92539	G02gh1	lipin 2	260.7493	235	297.151	264.3623	1.88E-01	-1.49E-01	1	Unchanged	Low
Q9NW01	G10gh3	hypothetical protein FLJ10402	165.6121	135	297.1276	199.1936	8.43E-01	-2.97E-01	1	Unchanged	Low
Q9NUW5	N21gh3	hypothetical protein FLJ10999	228.3252	247	297.5163	257.4882	3.82E-01	1.11E-01	1	Unchanged	Low
Q9BYC4	C13gh8	mitochondrial ribosomal protein S	478.9122	408	297.754	394.9285	-6.86E-01	-2.31E-01	1	Unchanged	Low
P02545	F01ab7	lamin A/C	707.7874	294	297.9921	433.306	-1.25E+00	-1.27E+00	1	Unchanged	Low
O60585	A17cd6	serine/arginine repetitive matrix	318.399	331	298.2057	315.9302	-9.45E-02	5.68E-02	1	Unchanged	Low
P23458	L12ef5	Janus kinase 1 (a protein tyrosin	385.7348	441	298.2124	375.1408	-3.71E-01	1.95E-01	1	Unchanged	Low
Q9BY13	O06gh8	hook3 protein	435.0319	471	298.2969	401.4116	-5.44E-01	1.14E-01	1	Unchanged	Low
Q9UBC2	C05gh5	epidermal growth factor receptor	171.9695	271	298.6179	247.3586	7.96E-01	6.59E-01	1	Unchanged	Low
O76022	A14cd7	E1B-55KDa-associated protein 5	256.9682	243	298.7615	266.0871	2.17E-01	-8.34E-02	1	Unchanged	Low
P33993	K04ef6	MCM7 minichromosome maintein	239.0601	165	298.875	234.4011	3.22E-01	-5.33E-01	1	Unchanged	Low
Q92963	F02cd2	Ric-like; expressed in many tissues	447.2008	499	299.9377	415.4004	-5.76E-01	1.58E-01	1	Unchanged	Low
Q9HAF1	P09gh5	hypothetical protein FLJ11730	270.4702	414	300.0397	328.0993	1.50E-01	6.13E-01	1	Unchanged	Low
Q9NZ36	P02gh4	uncharacterized hypothalamus p	505.7323	333	300.1219	379.485	-7.53E-01	-6.05E-01	1	Unchanged	Low
Q9BQQ3	C09gh8	golgi phosphoprotein 5	208.3671	343	300.1696	283.9342	5.27E-01	7.20E-01	1	Unchanged	Low
Q95214	P09ef3	leptin receptor overlapping trans-	292.4076	419	300.357	337.2896	3.87E-02	5.19E-01	1	Unchanged	Low
Q9Y294	A21ef8	DKFZP547E2110 protein	166.5906	243	301.1573	237.0749	8.54E-01	5.47E-01	1	Unchanged	Low
O95810	O01cd4	serum deprivation response (phc)	279.903	272	301.2133	284.3868	1.06E-01	-4.11E-02	1	Unchanged	Low
P30670	L21ab4	guanine nucleotide binding pro	470.8713	466	301.8899	412.8188	-6.41E-01	-1.59E-02	1	Unchanged	Low
P51946	O14ef5	cyclin H	180.4218	244	301.9337	242.2819	7.43E-01	4.38E-01	1	Unchanged	Low
O15290	G18cd1	retinoblastoma binding protein 6	298.4739	346	302.0906	315.4543	1.74E-02	2.12E-01	1	Unchanged	Low
Q9NX11	A03gh3	hypothetical protein FLJ20498	165.3845	190	302.1175	219.2418	8.69E-01	1.02E-01	1	Unchanged	Low
Q9P053	A23ef2	hypothetical protein LOC51240	187.2653	229	302.3118	239.5316	6.91E-01	2.90E-01	1	Unchanged	Low
P04554	H11ab8	proline 2	393.1528	362	302.3989	352.4183	-3.79E-01	-1.20E-01	1	Unchanged	Low
O15243	O05ef4	leptin receptor gene-related pro	329.3033	391	302.5417	340.9139	-1.22E-01	2.47E-01	1	Unchanged	Low
O43717	G03cd7	tumor differentially expressed 1	284.4848	364	302.9444	317.004	9.07E-02	3.54E-01	1	Unchanged	Low
O95876	J10ef1	hypothetical protein LOC51057	172.7128	226	302.9853	233.8891	8.11E-01	3.88E-01	1	Unchanged	Low
Q9HB05	N17gh5	tumor endothelial marker 6	247.105	190	303.4837	246.7925	2.96E-01	-3.81E-01	1	Unchanged	Low
Q9Y386	D24ef1	CGI-112 protein	493.6755	288	303.7855	361.6747	-7.01E-01	-7.80E-01	1	Unchanged	Low
Q9P057	E13ef2	hypothetical protein LDC51238	143.0704	139	303.8896	195.3392	1.09E+00	-4.11E-02	1	Unchanged	Low
O60630	D22ab4	delta homolog 1 (Drosophila)	310.6617	221	303.9702	278.4627	-3.14E-02	-4.93E-01	1	Unchanged	Low
O95285	O07gh1	macrophage erythroblast attachme	332.2343	413	304.0714	349.7511	-1.28E-01	3.14E-01	1	Unchanged	Low
Q08945	G17cd2	structure specific recognition pro	335.05	229	304.6617	289.639	-1.37E-01	-5.48E-01	1	Unchanged	Low
O43583	D08cd3	density-regulated protein	203.0088	253	304.7034	253.5145	5.86E-01	3.17E-01	1	Unchanged	Low
O95149	D04cd5	RNA: U transporter 1	186.979	254	304.889	248.5641	7.05E-01	4.41E-01	1	Unchanged	Low
Q9HAS8	N10gh4	elac homolog 2 (E. coli)	243.3076	331	304.8937	293.0254	3.26E-01	4.44E-01	1	Unchanged	Low
Q9BQ39	A23gh6	nucleolar protein GU2									

O15304	C06e6	CD27-binding (Siva) protein	88.75727	153	305.4708	182.3257	1.78E+00	7.83E-01	1	Unchanged	Low
Q15394	I08gh1	basic leucine-zipper protein BZA	347.7168	384	305.6252	345.6465	-1.86E-01	1.42E-01	1	Unchanged	Low
Q9NZ43	N09ef1	CDA14	235.1955	312	305.7623	284.2776	3.79E-01	4.07E-01	1	Unchanged	Low
P26022	P23ab8	pentraxin-related gene; rapidly in	97.61703	61.3	305.8598	154.9189	1.65E+00	-6.72E-01	1	Unchanged	Low
Q00536	L24ef5	PCTAIRE protein kinase 1	290.1914	359	306.0473	318.5577	7.68E-02	3.09E-01	1	Unchanged	Low
Q9JMW5	E19ef2	cerebral cell adhesion molecule	52.28353	234	306.6326	197.6582	2.55E+00	2.16E+00	1	Unchanged	Low
O95353	J17cd6	Cdc42 effector protein 3	95.65314	208	306.7186	203.4709	1.68E+00	1.12E+00	1	Unchanged	Low
O95808	B03ef2	arsenite resistance protein ARS-	187.799	225	307.4311	240.0311	7.11E-01	2.60E-01	1	Unchanged	Low
Q9BXJ8	O17gh8	transmembrane protein induced 1	411.8484	646	308.2116	455.5065	-4.18E-01	6.50E-01	1	Unchanged	Low
P38776	A06cd5	prolese; serine; 15	390.4608	365	308.5755	354.6324	-3.40E-01	9.78E-02	1	Unchanged	Low
Q9BUR5	M19gh6	hypothetical protein MGC4614	250.3191	338	308.7431	299.1204	3.03E-01	4.35E-01	1	Unchanged	Low
Q9Y3R1	F23cd6	Rab acceptor 1 (prenylated)	158.9446	207	308.7948	224.7776	9.58E-01	3.78E-01	1	Unchanged	Low
Q92997	D03ef7	dishevelled; dsh homolog 3 (Drosophila)	240.0941	305	309.2314	284.6254	3.65E-01	3.43E-01	1	Unchanged	Low
O14682	N17cd3	ectodermal-neural cortex (with B')	326.0664	189	309.539	274.7193	-7.50E-02	7.90E-01	1	Unchanged	Low
Q9Y255	I08cd8	px19-like protein	533.9588	455	309.7497	432.9739	-7.86E-01	2.30E-01	1	Unchanged	Low
Q16564	O17ef4	protein 'V1'	354.4762	286	310.2736	316.9703	-1.92E-01	3.09E-01	1	Unchanged	Low
P31943	O04ab7	heterogeneous nuclear ribonucleic acid	690.0051	250	310.5901	416.9005	-1.15E+00	-1.46E+00	1	Unchanged	Low
P49848	J09cd2	TAF6 RNA polymerase II; TATA	151.1422	133	310.9274	198.2917	1.04E+00	-1.87E-01	1	Unchanged	Low
Q04984	P19ab6	heat shock 70kD protein 1 (chaperone)	338.1568	327	311.1011	325.4422	-1.20E-01	-4.81E-02	1	Unchanged	Low
P20719	N08ef4	homeo box A5	271.1435	326	311.2742	302.8287	1.98E-01	2.63E-01	1	Unchanged	Low
Q9H5Y0	D21gh7	hypothetical protein FLJ22795	325.1674	305	311.3753	313.8457	-6.25E-02	-9.24E-02	1	Unchanged	Low
P19021	G15ab8	peptidylglycine alpha-amidating enzyme	219.5791	273	311.913	268.0943	5.06E-01	3.13E-01	1	Unchanged	Low
Q92544	B13gh1	KIAA0255 gene product	270.8313	307	312.0297	296.5662	2.04E-01	1.80E-01	1	Unchanged	Low
Q12907	G07cd7	chromosome 5 open reading frame	313.0938	222	312.5092	282.474	-2.70E-03	-4.97E-01	1	Unchanged	Low
Q9BW91	C03gh6	nudix (nucleoside diphosphate) kinase	346.395	314	312.5575	324.483	-1.48E-01	-1.35E-01	1	Unchanged	Low
P53365	M23cd8	partner of RAC1 (arfaptin 2)	293.2566	349	312.9335	318.382	9.37E-02	2.51E-01	1	Unchanged	Low
P58869	O17ab2	aryl hydrocarbon receptor	249.5731	417	313.1153	326.5306	3.27E-01	7.40E-01	1	Unchanged	Low
Q13145	I19cd8	putative transmembrane protein	490.8698	608	313.616	470.7589	-6.46E-01	3.08E-01	1	Unchanged	Low
O14747	A18ef6	death-associated protein 6	348.2382	450	313.7398	370.593	-1.51E-01	3.69E-01	1	Unchanged	Low
Q9GZT5	H03gh7	wingless-type MMTV integration site 1	362.0025	327	313.9764	334.369	-2.05E-01	-1.46E-01	1	Unchanged	Low
P08174	M19ef1	decay accelerating factor core 1	705.5781	457	314.0939	492.3204	-1.17E+00	-6.26E-01	1	Unchanged	Low
Q9H6B9	K01gh4	hypothetical protein RG083M05.1	241.9641	291	314.1855	282.3328	3.77E-01	2.65E-01	1	Unchanged	Low
Q9P077	K05ef2	hypothetical protein LOC51235	266.1575	324	314.3982	301.4061	2.40E-01	2.82E-01	1	Unchanged	Low
Q9H2V7	H12gh8	spinster-like protein	275.5997	394	314.4425	328.1261	1.88E-01	5.13E-01	1	Unchanged	Low
Q9NW70	D23gh2	hypothetical protein FLJ20625	420.6268	488	314.6523	407.636	-4.19E-01	2.13E-01	1	Unchanged	Low
Q9Y6X2	E22cd6	protein inhibitor of activated STAT	149.0425	237	315.0099	233.7882	1.08E+00	6.71E-01	1	Unchanged	Low
Q9P1P1	F10ef8	clone FLB172 (LOC51215)	419.8659	330	315.0092	355.1102	-4.15E-01	-3.46E-01	1	Unchanged	Low
P23919	H04cd7	deoxythymidine kinase (thymidine kinase)	123.4582	84.1	315.562	174.3854	1.35E+00	-5.53E-01	1	Unchanged	Low
P37140	D09ab8	protein phosphatase 1; catalytic	355.0781	503	315.7751	391.3748	-1.69E-01	5.03E-01	1	Unchanged	Low
Q9NW54	B22gh2	homolog of rat nadrin	432.3799	670	315.8314	472.8474	-4.53E-01	6.33E-01	1	Unchanged	Low
Q9UMS0	C05ef4	HIRA interacting protein 5	504.0153	382	315.8386	400.6081	-6.74E-01	-4.00E-01	1	Unchanged	Low
P14207	E23ef1	folate receptor 2 (fetal)	235.5291	154	316.0649	235.1893	4.24E-01	-6.13E-01	1	Unchanged	Low
Q9UJH7	L05ef4	makorin; ring finger protein; 1	243.752	243	316.3297	267.5313	3.76E-01	-7.36E-03	1	Unchanged	Low
Q75844	K23cd6	zinc metalloprotease (STE24 homolog)	338.221	174	316.3789	276.2357	-9.63E-02	-9.58E-01	1	Unchanged	Low
P18gh8	P18gh8	LIM homeobox protein 4	87.11814	84.8	316.6454	162.8523	1.86E+00	-3.90E-02	1	Unchanged	Low
P19ab2	P19ab2	ADP-ribosylation factor 3	444.3724	348	317.1873	369.9292	-4.86E-01	-3.52E-01	1	Unchanged	Low
Q9NY2Y	F18gh2	hypothetical protein FLJ10439	420.4716	399	317.2935	378.7795	-4.06E-01	-7.72E-02	1	Unchanged	Low
Q9Y3I1	J09ef4	F-box only protein 7	368.7457	422	317.6515	369.3121	-2.15E-01	1.93E-01	1	Unchanged	Low
Q9H320	P21cd8	variable charge; X chromosome	147.0814	348	318.4769	271.2531	1.11E+00	1.24E+00	1	Unchanged	Low
P49903	J11ef4	selenium donor protein	329.031	446	318.9322	364.5082	-4.50E-02	4.37E-01	1	Unchanged	Low
Q00506	B05cd6	serine/threonine kinase 25 (STE)	273.696	275	319.3179	289.4017	2.22E-01	7.86E-03	1	Unchanged	Low
Q00273	F14ab5	DNA fragmentation factor; 45 kDa	328.9933	401	319.634	350.0198	-4.16E-02	2.87E-01	1	Unchanged	Low
Q08170	H11cd2	splicing factor; arginine/serine-rich	231.1994	193	319.7733	247.9554	4.68E-01	-2.61E-01	1	Unchanged	Low
Q9Y3B8	N15ef8	small fragment nuclease	120.8094	282	320.0578	240.8904	1.41E+00	1.22E+00	1	Unchanged	Low
Q9P0N0	E11ef2	mitochondrial ribosomal protein L	377.6692	391	320.1382	362.9826	-2.38E-01	5.03E-02	1	Unchanged	Low
Q9BR13	D11gh8	hypothetical protein MGC11303.1	373.5695	391	320.4318	361.6895	-2.21E-01	6.60E-02	1	Unchanged	Low
Q9Y3I9	D19ef2	CGI-30 protein	107.1253	123	320.4576	183.4471	1.58E+00	1.97E-01	1	Unchanged	Low
Q16514	M17gh1	TAF12 RNA polymerase II; TATA	116.3618	304	320.8611	246.9777	1.46E+00	1.38E+00	1	Unchanged	Low
P13489	D13ef7	ribonuclease/angiogenin inhibitor	224.1663	232	320.8995	259.1076	5.18E-01	5.00E-02	1	Unchanged	Low
Q99987	P08ef5	vaccinia related kinase 2	205.9202	194	321.2364	240.3908	6.42E-01	-8.59E-02	1	Unchanged	Low
P56161	H21ef1	NADH dehydrogenase (ubiquinol oxidoreductase)	435.0715	319	321.3696	358.4382	-4.37E-01	-4.48E-01	1	Unchanged	Low
P51148	N18ab8	RAB5C; member RAS oncogene family	329.7976	358	321.5906	336.6203	-3.64E-02	1.20E-01	1	Unchanged	Low
Q9HD34	E12gh4	CGI-20 protein	257.866	249	322.3435	276.3612	3.22E-01	-5.12E-02	1	Unchanged	Low
Q9HAN2	F02gh6	pumilio homolog 2 (Drosophila)	291.9641	326	322.4096	313.4126	1.43E-01	1.58E-01	1	Unchanged	Low
P08107	I13ef5	heat shock 70kD protein 1A	535.4871	382	322.6223	413.3803	-7.31E-01	-4.87E-01	1	Unchanged	Low
O60499	N18cd3	syntaxin 10	189.7411	304	322.7738	272.2579	7.66E-01	6.81E-01	1	Unchanged	Low
Q9HB13	M19gh4	N-terminal kinase-like	165.2938	224	323.2472	237.4707	9.68E-01	4.38E-01	1	Unchanged	Low
Q9BSJ8	D22gh6	KIAA0747 protein	549.1645	575	323.5208	482.4222	-7.63E-01	6.53E-02	1	Unchanged	Low
O60838	G09gh7	SAC2 suppressor of actin mutation	216.0571	254	324.4643	264.8237	5.87E-01	2.33E-01	1	Unchanged	Low
Q9BTM6	M11gh8	hypothetical protein MGC3195.1	371.9412	334	324.5103	343.6424	-1.97E-01	-1.53E-01	1	Unchanged	Low
Q9H4L0	K06gh5	leucine zipper protein FK5K14	47.34403	70.6	324.6661	147.5387	2.78E+00	5.77E-01	1	Unchanged	Low
P50402	I14ab3	emerin (Emery-Dreifuss muscular dystrophy)	321.3743	304	324.6751	316.6654	1.47E-02	-8.04E-02	1	Unchanged	Low
Q9NZP7	G05ef3	calcium binding protein Cab45 p1	336.1107	239	324.6956	299.844	-4.98E-02	-4.94E-01	1	Unchanged	Low
P49116	B22cd2	nuclear receptor subfamily 2; group 5	295.9342	224	325.1253	281.6482	1.36E-01	-4.03E-01	1	Unchanged	Low
P11234	D14ab8	v-ras simian leukemia viral oncogene homolog 2	565.699	444	325.5924	444.9874	-7.97E-01	-3.51E-01	1	Unchanged	Low
P15408	D21ab5	FOS-like antigen 2	265.6989	437	325.8448	342.8236	2.94E-01	7.18E-01	1	Unchanged	Low
Q9P1Q8	N05cd8	RAB3A interacting protein (rabin-3)	357.8493	253	326.2784	312.2142	-1.33E-01	-5.03E-01	1	Unchanged	Low
P39060	P16ef6	collagen; type XVIII; alpha 1	151.6584	212	326.8288	230.0488	1.11E+00	4.81E-01	1	Unchanged	Low
Q9Y2N3	N05gh1	KIAA0618 gene product	378.8717	252	326.8347	319.0933	-2.13E-01	-5.91E-01	1	Unchanged	Low
P02749	M22ab2	apolipoprotein H (beta-2-glycoprotein)	408.7454	226	327.1228	320.758	-3.21E-01	-8.52E-01	1	Unchanged	Low
Q9P189	L20gh3	hypothetical protein PRO1855	392.3328	358	327.1908	359.0228	-2.62E-01	-1.34E-01	1	Unchanged	Low
O43822	B19ab4	chromosome 21 open reading frame	249.9987	297	327.8679	291.7148	3.91E-01	2.50E-01	1	Unchanged	Low
Q9UN22	N15ef2	likely ortholog of rat p47	413.5167	519	327.9429	420.0654	-3.35E-01	3.27E-01	1	Unchanged	Low
Q9Y4GS	B22cd8	dynein; cytoplasmic; heavy polypeptide	376.6624	426	327.9518	376.7971	-2.00E-01	1.77E-01	1	Unchanged	Low
Q13310	C13cd4	poly(A) binding protein; cytoplasmic	318.8746	338	328.1257	327.507	5.03E-02	9.11E-0			

P55317	A04ab7	hepatocyte nuclear factor 3; alph	273.7527	306	328.8562	302.8162	2.65E-01	1.60E-01	1 Unchanged Low
O43364	H16cd8	homeo box A2	511.053	468	329.292	435.9554	-6.35E-01	-1.28E-01	1 Unchanged Low
P55345	H15ab6	HMT1 hnRNP methyltransferase	364.8758	307	329.5023	333.8774	-1.47E-01	-2.48E-01	1 Unchanged Low
P48230	O22cd2	transmembrane 4 superfamily m	565.1635	417	330.825	437.5376	-7.73E-01	-4.40E-01	1 Unchanged Low
Q9BUY3	C21gh5	sorting nexin 6	166.5144	297	330.8949	264.7192	9.91E-01	8.34E-01	1 Unchanged Low
O00115	B01ef6	deoxyribonuclease II; lysosomal	275.2503	372	331.0554	326.0947	2.66E-01	4.34E-01	1 Unchanged Low
O43318	M11cd2	mitogen-activated protein kinase	186.7739	247	331.1308	254.8269	8.26E-01	4.01E-01	1 Unchanged Low
O95572	B08gh1	mitofusin 2	252.7846	277	331.4516	287.175	3.91E-01	1.33E-01	1 Unchanged Low
P35080	K12ab8	profilin 2	111.4363	85.9	332.2299	176.518	1.58E+00	-3.76E-01	1 Unchanged Low
Q9NW29	E24gh3	hypothetical protein FLJ10350	219.5611	173	332.8499	241.9521	6.00E-01	-3.40E-01	1 Unchanged Low
Q9NZE9	O07ef2	BRAF35/HDAC2 complex (80 kD	219.3916	348	332.8813	299.9861	6.01E-01	6.64E-01	1 Unchanged Low
Q9BYV2	C E05gh8	ring finger protein 30	500.2246	338	333.9675	390.6938	-5.83E-01	-5.66E-01	1 Unchanged Low
Q9UJX4	F02ef2	anaphase promoting complex sub	237.1218	269	334.5884	280.1684	4.97E-01	1.81E-01	1 Unchanged Low
O00302	B19cd6	calcium homeostasis endoplasm	327.1489	382	334.7371	347.7981	3.31E-02	2.22E-01	1 Unchanged Low
Q92866	K23cd1	neurogenin 1	290.2357	283	335.1054	302.7027	2.07E-01	-3.76E-02	1 Unchanged Low
O1429	P07cd3	histone acetyltransferase 1	344.9153	130	335.4301	270.1111	-4.02E-02	-1.41E+00	1 Unchanged Low
Q9NVK7	M18gh3	chromosome 19 open reading fra	281.2043	287	335.4383	301.1995	2.54E-01	2.92E-02	1 Unchanged Low
Q9UBN0	P09ef4	proline rich 3	309.5093	344	335.4526	329.7234	1.14E-01	1.50E-01	1 Unchanged Low
O43611	E14cd3	cytoplasmic linker 2	180.9108	220	336.1459	245.5832	8.94E-01	2.80E-01	1 Unchanged Low
Q94777	G23cd4	dichlorophosphate mannosyltran	294.1356	244	336.7183	291.5641	1.95E-01	-2.71E-01	1 Unchanged Low
Q14669	K05gh1	thyroid hormone receptor Interac	486.9829	397	337.0199	406.8782	-5.31E-01	-2.96E-01	1 Unchanged Low
Q9NUR0	B20gh3	hypothetical protein FLJ11196	63.09205	107	337.0769	168.9127	2.42E+00	7.56E-01	1 Unchanged Low
Q16822	L08ab8	phosphoenolpyruvate carboxykin	262.4601	156	337.1655	251.8272	3.61E-01	-7.52E-01	1 Unchanged Low
Q9Y640	A14cd8	stromal cell derived factor recept	215.2348	220	337.2906	257.3848	6.48E-01	2.92E-02	1 Unchanged Low
P48595	C01cd1	serine (or cysteine) proteinase In	62.04001	410	337.3872	269.7194	2.44E+00	2.72E+00	1 Unchanged Low
P26639	M15cd2	threonyl-tRNA synthetase	355.1309	422	337.8401	371.5003	-7.20E-02	2.47E-01	1 Unchanged Low
P29597	O03cd3	tyrosine kinase 2	209.3427	258	338.1471	268.5377	6.92E-01	3.02E-01	1 Unchanged Low
O60571	B02ab8	RAD1 homolog (S. pombe)	188.2716	104	339.1461	210.3983	8.49E-01	-8.59E-01	1 Unchanged Low
Q9NW97	P17gh2	hypothetical protein FLJ10199	262.3124	536	339.3086	379.0815	3.71E-01	1.03E+00	1 Unchanged Low
Q8P027	O23ef8	HSPC133 protein	616.0461	363	339.3102	439.5495	-8.60E-01	-7.62E-01	1 Unchanged Low
O95772	E20gh8	hypothetical protein MGC3251	195.5084	227	339.3644	254.0574	7.93E-01	2.12E-01	1 Unchanged Low
Q9NR28	N13gh4	second mitochondria-derived act	271.4457	543	339.8107	384.7351	3.24E-01	1.00E+00	1 Unchanged Low
P11413	F15ab3	glucose-6-phosphate dehydroge	258.0938	135	340.0217	244.4906	3.98E-01	-9.31E-01	1 Unchanged Low
Q99567	A04ab8	nudeoporfin 88kD	464.4826	320	340.5878	375.0149	-4.48E-01	-5.38E-01	1 Unchanged Low
Q9BZ9	F22gh7	ring finger protein 27	206.7918	398	340.7239	315.1764	7.20E-01	9.45E-01	1 Unchanged Low
O43632	L22cd6	gamma-tubuli complex protein z	328.0052	322	341.4805	330.4466	5.81E-02	2.73E-02	1 Unchanged Low
Q9Y305	I05cd8	Mitochondrial Acyl-CoA Thioester	447.9229	475	341.5085	421.5064	-3.91E-01	8.49E-02	1 Unchanged Low
P17096	L14ef6	high-mobility group (nonhistone	393.4158	266	341.5301	333.78	-2.04E-01	-5.62E-01	1 Unchanged Low
P28677	E10cd3	vitamin-like 1	235.283	241	341.6123	272.797	5.38E-01	3.76E-02	1 Unchanged Low
Q9UBX5	K04cd6	fbflin 5	79.52593	108	341.7638	176.4964	2.10E+00	4.44E-01	1 Unchanged Low
Q9Y304	E12er2	ovarian cancer overexpressed 1	326.0044	238	341.8947	301.8585	6.87E-02	-4.56E-01	1 Unchanged Low
O15379	L16ef6	histone deacetylase 3	198.0005	380	342.3529	306.8418	7.90E-01	9.41E-01	1 Unchanged Low
Q02790	H16ab5	FK506 binding protein 4 (59kD)	323.5993	240	343.4254	302.2597	5.85E-02	-4.33E-01	1 Unchanged Low
Q9H240	K12ef5	Notch homolog 2 (Drosophila)	270.5904	566	343.4339	393.3189	3.44E-01	1.06E+00	1 Unchanged Low
O76095	P22cd6	jumping translocation breakpoint	252.8696	227	343.482	274.4316	4.42E-01	-1.55E-01	1 Unchanged Low
Q9Y5Q8	P07cd7	general transcription factor IIIC; I	545.6403	324	343.9598	404.6602	-6.66E-01	-7.50E-01	1 Unchanged Low
Q9NW5	H06ef8	WD repeat domain 6	254.1607	369	344.0253	322.3381	4.37E-01	5.37E-01	1 Unchanged Low
P01121	C09ef4	ras homolog gene family; membe	241.7544	304	344.0732	296.4811	5.09E-01	3.29E-01	1 Unchanged Low
Q9H0V7	K18gh8	hypothetical protein DKFZp564O	568.248	304	344.2985	405.6584	-7.23E-01	-9.00E-01	1 Unchanged Low
O60664	P02cd5	cargo selection protein (mannose	520.0919	232	344.5523	365.5782	-5.94E-01	-1.16E+00	1 Unchanged Low
P56554	O15cd3	ubiquitin-conjugating enzyme E2	374.4383	417	345.0269	378.959	-1.18E-01	1.57E-01	1 Unchanged Low
O00330	O06cd3	Pyruvate dehydrogenase comple	345.9372	430	345.2213	373.6892	-2.99E-03	3.14E-01	1 Unchanged Low
O60784	N17cd5	target of myb1 (chicken)	364.3098	317	345.2431	342.086	-7.76E-02	-2.02E-01	1 Unchanged Low
Q9NQZ0	H03ef4	CMP-N-acetylneuraminic acid sy	788.5176	339	345.3498	491.0715	-1.19E+00	-1.22E+00	1 Unchanged Low
P52790	A04ab5	hexokinase 3 (white cell)	260.6034	430	345.4621	345.2169	4.07E-01	7.21E-01	1 Unchanged Low
P52815	B10cd1	mitochondrial ribosomal protein l	234.3191	277	345.7776	285.7775	5.61E-01	2.43E-01	1 Unchanged Low
O14983	O10ef1	ATPase; Ca++ transporting; card	167.4066	223	346.1734	245.4613	1.05E+00	4.12E-01	1 Unchanged Low
P04259	D01ab7	keratin 6B	534.1837	405	347.6543	428.9832	-6.20E-01	-3.99E-01	1 Unchanged Low
P16455	M04ef6	O-6-methylguanine-DNA methyl	299.0887	307	348.0545	318.0812	2.19E-01	3.81E-02	1 Unchanged Low
Q9Y5L9	N04cd6	Snf2-related CBP activator prote	285.2875	187	348.0925	273.2945	2.87E-01	-6.13E-01	1 Unchanged Low
P41214	A16gh1	lilalin	237.0742	307	348.5538	297.4677	5.56E-01	3.72E-01	1 Unchanged Low
Q9H6U4	P13gh5	hypothetical protein FLJ21865	419.2747	175	348.8375	314.4039	-2.65E-01	-1.26E+00	1 Unchanged Low
Q15393	L10ef7	splicing factor 3b; subunit 3; 130	242.1115	239	349.6571	277.0735	5.30E-01	-1.59E-02	1 Unchanged Low
P55055	C04gh1	nuclear receptor subfamily 1; grp	325.6291	368	349.8393	347.7942	1.03E-01	1.76E-01	1 Unchanged Low
P51805	M03ef4	SEX gene	303.0664	383	350.6414	345.4093	2.10E-01	3.36E-01	1 Unchanged Low
O75815	G23ab3	breast cancer anti-estrogen resis	249.1903	293	350.9571	297.768	4.94E-01	2.34E-01	1 Unchanged Low
Q9Y2Y9	F19ef2	Kruppel-like factor 13	241.1753	366	351.0501	319.2905	5.42E-01	6.00E-01	1 Unchanged Low
Q99633	D04cd3	pre-mRNA processing factor 18	405.0464	348	351.3478	368.1888	-2.05E-01	-2.18E-01	1 Unchanged Low
P05155	C08ab3	serine (or cysteine) proteinase in	303.3386	334	351.5074	329.7432	2.13E-01	1.41E-01	1 Unchanged Low
Q9UN5	O16cd7	EAP30 subunit of ELL complex	321.8045	326	351.5535	333.1657	1.27E-01	1.84E-02	1 Unchanged Low
Q14011	E11ab4	cold inducible RNA binding prote	292.5107	412	351.6685	352.0144	2.66E-01	4.94E-01	1 Unchanged Low
O75807	M02ef3	protein phosphatase 1; regulator	371.7509	652	352.5048	458.6852	-7.67E-02	8.10E-01	1 Unchanged Low
Q14457	K19ab3	beclin 1 (coiled-coil); myosin-like	368.4142	678	352.9542	466.4393	-6.18E-02	8.80E-01	1 Unchanged Low
Q02818	J06ef6	nucleobindin 1	330.8747	213	353.1168	298.8382	9.39E-02	-6.39E-01	1 Unchanged Low
O15235	L10gh1	mitochondrial ribosomal protein s	355.1234	467	353.2438	391.6738	-7.66E-03	3.94E-01	1 Unchanged Low
Q9Y3E0	A02ef2	CGI-141 protein	152.8668	320	353.6986	275.4907	1.21E+00	1.07E+00	1 Unchanged Low
Q9NQZ5	H19gh4	START domain containing 7	277.2941	280	353.7264	303.5369	3.51E-01	1.19E-02	1 Unchanged Low
Q9UHW4	D24ef8	protein x 0001	266.9848	291	353.7644	303.9535	4.06E-01	1.25E-01	1 Unchanged Low
P82914	P04gh7	mitochondrial ribosomal protein s	444.1517	417	354.4965	405.0567	-3.25E-01	-9.27E-02	1 Unchanged Low
P25787	L11ef7	proleasome (prosome; macropal	432.9379	528	355.1116	437.9448	-2.86E-01	2.80E-01	1 Unchanged Low
P28447	D02cd1	S100 calcium binding protein A4	198.7401	273	355.1396	275.5734	8.38E-01	4.57E-01	1 Unchanged Low
Q9Y605	P02gh8	T-cell activation protein	411.1148	356	355.1531	373.9358	-2.11E-01	-2.10E-01	1 Unchanged Low
Q14776	K14cd4	leucine-zipper-like transcriptiona	202.0365	273	355.4522	276.788	8.15E-01	4.34E-01	1 Unchanged Low
P30837	C02ab2	aldehyde dehydrogenase 1 fami	631.0407	451	355.7998	479.1158	-8.27E-01	-4.86E-01	1 Unchanged Low
P09668	L03ef7	cathepsin H	460.8488	564	356.7735	460.5856	-3.69E-01	2.92E-01	1 Unchanged Low
Q02313	J02gh8	Krueppel-related zinc finger prot	402.289	391	356.9162	383.4797	-1.73E-01	-4.02E-02	1 Unchanged Low

Q13148	H11cd7	TAR DNA binding protein	322.5816	353	357.1404	344.328	1.47E-01	1.31E-01	1 Unchanged Low
Q16645	K24ab5	FK506 binding protein 1B (12.6 kDa)	216.7704	486	357.2698	353.4204	7.21E-01	1.17E+00	1 Unchanged Low
	N02gh8	protein phosphatase 1; regulator	77.52993	71.1	357.2714	168.643	2.20E+00	-1.24E-01	1 Unchanged Low
P57739	F18gh1	claudin 2	188.162	238	357.443	261.2968	9.26E-01	3.41E-01	1 Unchanged Low
O60568	F13cd4	procollagen-lysine-2-oxoglutarate	332.5306	269	357.5594	319.8117	1.05E-01	-3.04E-01	1 Unchanged Low
Q9HAU4	N11gh5	E3 ubiquitin ligase SMURF2	425.5948	665	357.6911	482.7167	-2.51E-01	6.44E-01	1 Unchanged Low
P49914	J01cd6	5,10-methenyltetrahydrofolate synthetase	340.2344	238	358.026	312.027	7.38E-02	-5.17E-01	1 Unchanged Low
O60510	E11cd8	atrophin-1 interacting protein 1; :;	171.9425	265	358.342	265.2168	1.06E+00	6.26E-01	1 Unchanged Low
Q9BX68	L15gh8	histidine triad nucleotide binding	207.0703	360	358.5328	308.6409	7.92E-01	7.99E-01	1 Unchanged Low
P29084	B02ab5	general transcription factor II E; p	261.3572	225	358.821	281.687	4.57E-01	-2.17E-01	1 Unchanged Low
P09526	C05ef6	RAP1B; member of RAS oncogene	320.4156	355	359.0861	344.9493	1.64E-01	1.49E-01	1 Unchanged Low
O15471	P01ef4	leukocyte immunoglobulin-like receptor	219.8277	260	359.2909	279.8225	7.09E-01	2.44E-01	1 Unchanged Low
Q9UEEB	K03ab3	craniofacial development protein	124.0304	245	359.5047	242.684	1.54E+00	9.79E-01	1 Unchanged Low
Q15011	L03ef3	homocysteine-inducible endoplasmic reticulum protein	352.4459	183	359.7095	298.5074	2.94E-02	-9.43E-01	1 Unchanged Low
Q9BWG8	A13gh8	hypothetical protein MGC2491	170.1162	203	360.534	244.6389	1.08E+00	2.57E-01	1 Unchanged Low
Q9Y397	A04ef2	Zinc finger; DHC domain contain	431.1743	495	360.6182	428.8727	-2.58E-01	1.99E-01	1 Unchanged Low
Q14598	H17ab7	membrane component; chromosom	303.2476	402	361.5265	355.7499	2.54E-01	4.08E-01	1 Unchanged Low
P23497	C13cd2	nuclear antigen Sp100	331.8296	491	361.9825	394.8464	1.25E-01	5.84E-01	1 Unchanged Low
Q16633	A24cd1	POU domain; class 2; associatin	103.1231	99.3	362.0007	188.1549	1.81E+00	-5.33E-02	1 Unchanged Low
Q99881	J12cd1	SH3-domain GRB2-like 1	231.086	247	362.8536	280.235	6.51E-01	9.47E-02	1 Unchanged Low
Q70201	N20ab3	complement component 1; q subunit	471.8742	202	363.3385	345.9018	-3.77E-01	-1.22E+00	1 Unchanged Low
Q16513	E04cd1	protein kinase C-like 2	546.0111	561	364.4852	490.5792	-5.83E-01	3.97E-02	1 Unchanged Low
Q9H070	H10cd8	adaptor-related protein complex 2	353.2901	278	364.7541	331.9695	4.61E-02	-3.46E-01	1 Unchanged Low
Q13227	A16ab5	G protein pathway suppressor 2	557.5311	352	364.8449	424.6909	-6.12E-01	-6.65E-01	1 Unchanged Low
P20339	M03ef5	RAB5A; member RAS oncogene	404.6579	664	365.7139	478.1731	-1.46E-01	7.15E-01	1 Unchanged Low
Q9NX44	G15gh2	hypothetical protein FLJ20005	155.2731	246	365.9622	255.5867	1.24E+00	6.61E-01	1 Unchanged Low
Q9Z900	N17cd1	regulator of nonsense transcripts	328.2926	316	366.2931	336.7297	1.58E-01	-5.69E-02	1 Unchanged Low
Q9H2K4	I05gh3	chromosome 11 open reading frame	198.6548	155	366.4866	240.051	8.83E-01	-3.58E-01	1 Unchanged Low
O14917	E17ef4	protocadherin 17	250.3859	311	366.6879	309.398	5.50E-01	3.13E-01	1 Unchanged Low
Q9NZ88	J06gh3	chromosome 6 open reading frame	199.6701	362	367.2681	309.7781	8.79E-01	8.60E-01	1 Unchanged Low
Q9BYC8	C15gh8	mitochondrial ribosomal protein L	257.9414	429	367.9727	351.4981	5.13E-01	7.33E-01	1 Unchanged Low
Q15311	C21cd7	radial arm protein 1	295.4648	411	368.6028	358.3107	3.19E-01	4.76E-01	1 Unchanged Low
Q9NW9	E02gh3	hypothetical protein FLJ10074	455.3747	383	369.4489	402.6031	-3.02E-01	-2.50E-01	1 Unchanged Low
O95571	G22ef3	protein expressed in thyroid	398.0124	507	369.925	425.0962	-1.06E-01	3.50E-01	1 Unchanged Low
P36941	A09ab7	lymphoid tyrosine receptor (TNFR)	403.0565	454	370.0343	409.094	-1.23E-01	1.72E-01	1 Unchanged Low
P49790	F11cd5	nucleoporin 153kD	264.6175	316	370.2793	317.116	4.65E-01	2.58E-01	1 Unchanged Low
Q99607	C06ab4	E74-like factor 4 (ets domain) trar	267.1335	268	371.3515	302.1703	4.75E-01	4.79E-03	1 Unchanged Low
Q9JUV1	H05cd8	CCR4-NOT transcription complex	201.0959	465	371.6771	345.9619	8.86E-01	1.21E+00	1 Unchanged Low
Q9Y3E4	O13ef2	CG146 protein	107.5317	262	371.8333	247.1535	1.79E+01	1.29E+00	1 Unchanged Low
P19367	D17ab3	hexokinase 1	512.0647	215	371.9817	366.4437	-4.61E-01	-1.25E+00	1 Unchanged Low
Q14250	J15cd5	enigma (LIM domain protein)	229.1944	218	371.9927	272.9152	6.99E-01	-7.52E-02	1 Unchanged Low
Q9UL33	B20ef2	unknown	343.1533	636	372.4427	450.4535	1.18E-01	8.90E-01	1 Unchanged Low
Q15019	H03ef5	neural precursor cell expressed;	489.0601	274	372.9279	378.666	-3.91E-01	-8.36E-01	1 Unchanged Low
Q13084	H05cd6	melanoma-associated antigen re	421.8259	278	373.0512	357.6504	-1.77E-01	-6.01E-01	1 Unchanged Low
Q9JUMR2	O18cd7	DEAD/H (Asp-Glu-Ala-Glu/His) tr	383.654	423	373.0622	393.1434	-4.04E-02	1.40E-01	1 Unchanged Low
P55855	H06cd2	SMT3 suppressor of mif tw 3 hr	454.9011	444	373.596	424.0867	-2.84E-01	-3.58E-02	1 Unchanged Low
Q13155	G20cd4	J17V1 gene	322.6641	409	373.7416	368.4293	2.12E-01	3.42E-01	1 Unchanged Low
P78371	H11cd6	chaperonin containing TCP1; sub	480.5464	430	374.014	428.2475	-3.62E-01	-1.60E-01	1 Unchanged Low
P08173	P17ab3	cholinergic receptor; muscarinic	444.2461	514	374.4117	444.3189	-2.47E-01	2.11E-01	1 Unchanged Low
O60478	E02cd2	transmembrane 7 superfamily me	274.7639	438	374.61	362.4988	4.47E-01	6.73E-01	1 Unchanged Low
O60429	D16gh4	hypothetical protein FLJ12886	142.8322	257	375.0573	258.282	1.39E+00	8.47E-01	1 Unchanged Low
O75935	O04cd7	dynactin 3 (p22)	408.9696	432	375.1224	405.4281	-1.25E-01	7.97E-02	1 Unchanged Low
Q13147	J05ab2	abl-interactor 2	299.098	249	375.379	307.9098	3.28E-01	-2.63E-01	1 Unchanged Low
Q9NPH4	E14gh3	LUC7-like (S. cerevisiae)	207.38	302	376.3768	295.4166	8.60E-01	5.45E-01	1 Unchanged Low
Q9UJ96	C13cd8	potassium voltage-gated channel	582.717	448	376.4373	468.9343	-6.30E-01	-3.80E-01	1 Unchanged Low
P17081	C13ef6	likely ortholog of mouse TC10-alk	293.1604	417	376.4996	362.2816	3.61E-01	5.09E-01	1 Unchanged Low
P11166	J05ef5	solute carrier family 2 (facilitated	351.7333	393	376.564	373.8343	9.84E-02	1.61E-01	1 Unchanged Low
Q14820	D12ef6	splicing factor 1	382.846	408	376.7779	389.2167	-2.30E-02	9.19E-02	1 Unchanged Low
Q92935	I06ab5	exostoses (multiple)-like 1	659.9005	276	376.8548	437.6869	-8.08E-01	-1.25E+00	1 Unchanged Low
P31749	E20ef6	v-akt murine thymoma viral oncogene	385.4669	303	376.9169	355.1851	-3.24E-02	-3.46E-01	1 Unchanged Low
Q13454	L05cd7	Putative prostate cancer tumor suppressor	326.9146	363	377.0852	355.5691	2.08E-01	1.50E-01	1 Unchanged Low
P35520	C24ab3	cystathione-beta-synthase	70.85109	68.1	377.1148	172.0203	2.41E+00	-5.72E-02	1 Unchanged Low
P53602	M01ab7	mevalonate (diphospho) decarboxylase	682.0309	178	378.114	412.6357	-8.51E-01	-1.94E-00	1 Unchanged Low
Q9H7G3	C04gh6	mitochondrial ribosomal protein L	333.6677	207	378.1398	306.3867	1.81E-01	-8.66E-01	1 Unchanged Low
Q13123	C06ab7	IK cytokine; down-regulator of H1	257.7332	439	378.1808	358.3458	5.53E-01	7.69E-01	1 Unchanged Low
O14744	G14cd6	SKB1 homolog (S. pombe)	348.0026	410	378.4165	378.8177	1.21E-01	2.37E-01	1 Unchanged Low
Q9Y566	D16ef8	SH3 and multiple ankyrin repeat	209.2687	281	378.5197	290.0718	8.59E-01	4.27E-01	1 Unchanged Low
Q9BLU9	A03gh7	Mov10; Moloney leukemia virus	385.0517	472	380.308	412.4352	-1.79E-02	2.94E-01	1 Unchanged Low
P51730	I02ab5	chloride channel 3	330.2251	237	380.3105	315.7621	2.04E-01	-4.80E-01	1 Unchanged Low
O14547	J09cd6	PRP8 pre-mRNA processing fact	239.0005	256	380.5886	291.9777	6.71E-01	1.01E-01	1 Unchanged Low
Q99753	A05cd7	clspn1 resistance associated	257.1873	397	380.7894	345.0384	5.66E-01	6.27E-01	1 Unchanged Low
Q9NQC8	H15gh4	hypothetical protein LOC56912	185.2607	276	381.0416	280.7773	1.04E+00	5.75E-01	1 Unchanged Low
O43919	M01ef6	linker for activation of T cells	206.6585	105	381.2059	230.823	8.83E-01	-9.82E-01	1 Unchanged Low
P78345	F15cd6	ribonuclease P (38kD)	321.791	530	381.5687	411.2575	2.46E-01	7.21E-01	1 Unchanged Low
PS4257	A03ef5	huntingtin-associated protein 1 (I)	450.2874	322	382.6029	384.9948	-2.35E-01	-4.83E-01	1 Unchanged Low
Q9Y3F4	G18cd7	unr-interacting protein	390.9437	335	382.6142	369.3734	-3.11E-02	-2.25E-01	1 Unchanged Low
P29536	F14cd7	leiomodin 1 (smooth muscle)	343.3731	209	382.9438	311.936	1.57E-01	7.13E-01	1 Unchanged Low
O75925	K03cd4	protein inhibitor of activated STA	423.9992	606	383.7943	471.2944	-1.44E-01	5.15E-01	1 Unchanged Low
Q9UMX5	J23ef4	secreted protein of unknown func	344.8668	306	384.5676	345.2233	1.57E-01	-1.71E-01	1 Unchanged Low
Q9UMZ9	N02cd7	Interleukin enhancer binding fact	348.7866	278	384.7729	337.1554	1.42E-01	-3.28E-01	1 Unchanged Low
Q92905	P03ef6	COP9 constitutive photomorphog	257.5597	392	386.1452	345.1985	5.84E-01	6.06E-01	1 Unchanged Low
Q9NSD7	L20ef1	G-protein coupled receptor SALF	734.6282	277	386.7193	466.2798	-9.26E-01	-1.40E+00	1 Unchanged Low
Q9P2W3	G01ef3	guanine nucleotide binding prote	70.71144	81.4	386.7442	179.6321	2.45E+00	2.04E-01	1 Unchanged Low
Q9BV7	N14gh5	mitochondrial ribosomal protein S	367.7177	520	386.9198	424.8293	7.34E-02	4.99E-01	1 Unchanged Low
Q9Y4L1	B23cd8	oxygen regulated protein (150kD	413.0575	372	387.5372	390.9975	-9.20E-02	-1.49E-01	1 Unchanged Low
Q92363	F18ab7	Inhibitor of DNA binding 2; domfr	484.7132	359	388.2552	410.6421	-3.20E-01	-4.33E-01	1 Unchanged Low

Q9Y5J8	E06cd8	translocase of inner mitochondria	440.2763	542	388.4554	456.8557	-1.81E-01	2.99E-01	1	Unchanged Low
	E22ef1	G protein-coupled receptor 26	499.1316	450	389.582	446.2248	-3.57E-01	-1.50E-01	1	Unchanged Low
Q99501	N11cd6	growth arrest-specific 2 like 1	359.8065	540	389.6398	429.6515	1.15E-01	5.84E-01	1	Unchanged Low
Q00613	M17ef5	heat shock transcription factor 1	363.3847	375	389.8695	376.2292	1.01E-01	4.71E-02	1	Unchanged Low
Q9H5Z1	H16gh4	DEAD/H (Asp-Glu-Ala-Asp/His) t	136.5899	124	389.9335	217.0007	1.51E+00	-1.35E-01	1	Unchanged Low
P09661	P24cd1	small nuclear ribonucleoprotein p	441.1409	115	390.2085	315.5701	-1.77E-01	-1.94E+00	1	Unchanged Low
P54709	P05ef5	ATPase; Na+/K+ transporting; bc	425.6647	432	391.8135	416.5779	-1.20E-01	2.22E-02	1	Unchanged Low
P13164	M06ef5	interferon induced transmembrane	45.13817	256	392.1204	231.1336	3.12E+00	2.50E+00	1	Unchanged Low
Q9Y6E2	A23ef8	HSPC028 protein	329.8857	363	392.2431	361.6248	2.50E-01	1.37E-01	1	Unchanged Low
Q9NVG2	B13gh3	vacuolar protein sorting 35 (yea	359.0233	557	392.2574	436.0959	1.28E-01	6.34E-01	1	Unchanged Low
P27448	E10ef5	MAP/microtubule affinity-regula	397.7845	369	392.3918	386.4633	-1.97E-02	-1.08E-01	1	Unchanged Low
O15438	P18cd3	ATP-binding cassette; sub-family	618.0409	488	392.8159	499.6643	-6.54E-01	-3.40E-01	1	Unchanged Low
Q9UL48	I04ef2	Ck2 interacting protein 1; HQ002	176.5553	215	393.4111	261.8209	1.16E+00	2.88E-01	1	Unchanged Low
Q94763	A11cd4	RPB5-mediating protein	333.8215	533	393.9448	420.3384	2.40E-01	6.77E-01	1	Unchanged Low
Q13190	H19cd2	synlaxin 5A	179.6146	235	393.985	269.5995	1.13E+00	3.89E-01	1	Unchanged Low
Q13222	D21ef3	EBNA-2 co-activator (100kD)	381.3069	303	394.5999	383.7948	4.94E-02	-2.22E-02	1	Unchanged Low
O75312	L01cd4	zinc finger protein 259	348.7542	422	394.8016	388.3905	1.79E-01	2.74E-01	1	Unchanged Low
P37837	D20cd2	transaldolase 1	399.2717	328	395.693	373.7275	-1.30E-02	-2.92E-01	1	Unchanged Low
O75762	G19cd6	ankyrin-like with transmembrane	222.8517	364	395.7427	327.3962	8.28E-01	7.06E-01	1	Unchanged Low
Q99569	K19ef3	retinoic acid receptor responder	283.5705	257	396.0287	312.0672	4.82E-01	-1.44E-01	1	Unchanged Low
Q9UNP2	H15cd2	solute carrier family 1 (neutral an	149.1019	138	396.5014	227.7665	1.41E+00	-1.15E-01	1	Unchanged Low
P56524	C23cd6	histone deacetylase 4	328.6037	303	397.1317	342.9334	2.73E-01	-1.17E-01	1	Unchanged Low
Q9H644	C19gh6	hypothetical protein MGC5585	140.9811	228	397.2624	255.3931	1.49E-01	6.93E-01	1	Unchanged Low
Q13627	O19ab4	dual-specificity tyrosine-(Y)-phos	498.484	327	397.3922	407.7774	-3.27E-01	-6.06E-01	1	Unchanged Low
Q03405	O01ef5	plasmogen activator; uridyl kinase	500.1391	395	398.2456	431.3524	-3.29E-01	-3.38E-01	1	Unchanged Low
Q9NPQ8	L18gh4	likely ortholog of mouse synembry	372.6251	443	398.4083	404.6217	9.57E-02	2.48E-01	1	Unchanged Low
Q15375	A10ab5	EphA7	243.0574	290	398.5414	310.5659	7.13E-01	2.55E-01	1	Unchanged Low
P05114	G04ab7	high-mobility group (nonhistone)	198.8334	278	398.7327	291.2748	1.02E+00	4.99E-01	1	Unchanged Low
Q9UKU4	C13ef2	retinal short-chain dehydrogenase	370.8225	497	399.4413	422.4244	1.07E-01	4.23E-01	1	Unchanged Low
P08195	E21ab7	solute carrier family 3 (activators	442.5453	345	399.5578	395.768	-1.47E-01	-3.58E-01	1	Unchanged Low
Q15545	J11cd2	TAF7 RNA polymerase II; TATA	400.689	526	401.1303	442.5426	1.59E-03	3.92E-01	1	Unchanged Low
	D24gh8	hypothetical protein FLJ14511	246.3293	225	401.3816	290.8781	7.04E-01	-1.31E-01	1	Unchanged Low
Q05397	L20ef5	PTK2 protein tyrosine kinase 2	389.8718	440	401.4713	410.2909	4.23E-02	1.73E-01	1	Unchanged Low
Q9Y6G1	C21ef8	PTD011 protein	434.6906	483	401.5119	439.8467	-1.15E-01	1.53E-01	1	Unchanged Low
P41212	O23ef5	ets variant gene 6 (TEL oncogene	315.7331	502	401.8424	406.6035	3.49E-01	6.70E-01	1	Unchanged Low
O14737	G05cd5	programmed cell death 5	498.729	430	402.3091	443.7457	-3.10E-01	-2.13E-01	1	Unchanged Low
Q9UHB9	A10ef3	signal recognition particle 68kD	212.5357	247	402.3276	287.2236	9.21E-01	2.16E-01	1	Unchanged Low
Q96D21	C20el8	RASD family; member 2	395.909	486	402.4304	427.9499	2.36E-02	2.94E-01	1	Unchanged Low
Q9Y411	J05ef1	myosin VA (heavy polypeptide 1)	371.5954	353	402.453	375.8247	1.15E-01	-7.23E-02	1	Unchanged Low
Q9Y5L4	L14ef7	translocase of inner mitochondria	291.7019	369	404.0738	354.9111	4.70E-01	3.39E-01	1	Unchanged Low
O75439	N22cd4	peptidase (mitochondrial process	512.9004	184	404.5715	367.0789	-3.42E-01	-1.48E+00	1	Unchanged Low
P55010	K22ab4	eukaryotic translation initiation fa	427.4989	296	405.4995	376.3076	-7.62E-02	-5.31E-01	1	Unchanged Low
Q9BY44	G10gh8	CDA2 protein	453.6064	401	405.956	420.1404	-1.60E-01	-1.78E-01	1	Unchanged Low
Q13164	B21ef5	mitogen-activated protein kinase	209.1026	256	406.234	290.5304	9.58E-01	2.93E-01	1	Unchanged Low
P53667	P08ab6	LIM domain kinase 1	359.4655	392	406.5183	386.0829	1.77E-01	1.26E-01	1	Unchanged Low
Q9UNH6	F05ef2	sorting nexin 7	479.6898	396	406.7812	427.3762	-2.38E-01	-2.78E-01	1	Unchanged Low
O00258	K17cd4	tryptophan rich basic protein	339.3172	500	407.1504	415.5431	2.63E-01	5.60E-01	1	Unchanged Low
Q9Y310	H12ef3	hypothetical protein	458.2693	546	407.2408	470.3717	-1.70E-01	2.52E-01	1	Unchanged Low
Q9Y368	D13cd8	parvin; beta	114.232	159	407.3882	226.9908	1.83E+00	4.80E-01	1	Unchanged Low
P14866	H13ab6	heterogeneous nuclear ribonucle	442.5489	274	407.4025	374.6383	-1.19E-01	-6.92E-01	1	Unchanged Low
Q13885	K01cd3	tubulin; beta polypeptide	441.2669	413	407.8583	420.8456	-1.14E-01	-9.41E-02	1	Unchanged Low
O43765	J06cd1	small glutamine-rich tetrapeptide	378.9705	438	408.6453	408.6939	1.09E-01	2.10E-01	1	Unchanged Low
O14632	B12ef4	homeodomain interacting protein	394.449	535	408.8773	446.1081	5.18E-02	4.40E-01	1	Unchanged Low
P19339	L10ab2	5-aminolevulinate delta-carboxylate	501.3028	386	409.3069	432.286	-2.92E-01	-3.76E-01	1	Unchanged Low
P28331	P18ab8	NADH dehydrogenase (ubiquinol	490.4347	417	409.3283	438.7901	-2.61E-01	-2.35E-01	1	Unchanged Low
P41970	P05ef6	ELK3; ETS-domain protein (SRF	205.9453	359	410.8037	325.3706	9.96E-01	8.03E-01	1	Unchanged Low
Q92973	J22ab6	karyopherin (importin) beta 2	393.6551	234	410.9425	346.1733	6.20E-02	-7.51E-01	1	Unchanged Low
P36507	J10ef5	mitogen-activated protein kinase	395.22	437	411.4052	414.6953	5.79E-02	1.46E-01	1	Unchanged Low
Q16515	F21ab8	protein kinase C-like 1	456.2727	486	411.8245	451.4528	-1.48E-01	1.98E-02	1	Unchanged Low
O43447	M08cd6	peptidyl prolyl isomerase H (cycl	179.441	222	411.9165	271.0162	1.20E+00	3.05E-01	1	Unchanged Low
P30040	M13ef3	chromosome 12 open reading fra	346.6792	296	412.2064	351.5665	2.50E-01	-2.29E-01	1	Unchanged Low
O95399	C19cd7	urokinase 2	452.0721	366	413.1451	410.4914	-1.30E-01	-3.04E-01	1	Unchanged Low
	M01ab3	UDP-Gal-betaGal beta 1;3-galac	499.5929	290	413.3454	401.0113	-2.74E-01	-7.87E-01	1	Unchanged Low
Q12792	N11ab8	protein tyrosine kinase 9	476.3952	364	413.4208	418.007	-2.05E-01	-3.87E-01	1	Unchanged Low
Q14318	J02cd7	FK506 binding protein 6 (38kD)	461.2322	432	413.4238	435.6453	-1.58E-01	-9.35E-02	1	Unchanged Low
O75955	N10cd5	flotillin 1	304.6674	310	415.4364	343.496	4.47E-01	2.68E-02	1	Unchanged Low
Q9BVY8	B09gh7	hypothetical protein MGC5499	490.2382	417	416.02	440.9559	-2.37E-01	-2.35E-01	1	Unchanged Low
Q16288	O19ef5	neurotrophic tyrosine kinase; rec	126.7467	186	416.4128	243.0358	1.72E+00	5.53E-01	1	Unchanged Low
Q75380	J20ab8	NADH dehydrogenase (ubiquinol	449.5778	413	416.4836	462.4999	-1.10E-01	-1.21E-01	1	Unchanged Low
Q9BVY1	B15gh8	hypothetical protein GL009	429.1998	354	417.3575	400.0464	-4.04E-02	-2.80E-01	1	Unchanged Low
Q9BVK3	E19gh6	hypothetical protein MGC2463	462.5828	387	417.7046	422.5145	-1.47E-01	-2.56E-01	1	Unchanged Low
Q9P0N3	A24ef2	hypothetical protein FLJ10597	137.7487	289	417.999	281.424	1.60E+00	1.07E+00	1	Unchanged Low
P24534	D03ab4	eukaryotic translation elongation	347.2405	328	418.0152	364.5026	2.68E-02	-9.11E-02	1	Unchanged Low
P49336	C01ab4	cyclin-dependent kinase 8	426.3751	281	418.121	375.2575	-2.82E-02	-6.00E-01	1	Unchanged Low
P34130	P16cd2	neurotrophin 5 (neurotrophin 4/5'	327.4146	223	418.6011	323.0643	3.54E-01	-5.53E-01	1	Unchanged Low
O75425	P06gh5	hypothetical protein AF053356	340.4357	339	419.3637	366.1692	3.01E-01	-7.34E-03	1	Unchanged Low
Q15293	F16ab8	reluculocalbin 1; EF-hand calcium	241.6383	250	420.5597	304.1243	7.99E-01	5.01E-02	1	Unchanged Low
O95376	D08ab2	arafide homolog 2 (Drosophila)	254.1122	322	420.8229	332.2465	7.28E-01	3.41E-01	1	Unchanged Low
O75489	J16ab8	NADH dehydrogenase (ubiquinol	375.7034	327	422.3772	375.1108	1.69E-01	-1.99E-01	1	Unchanged Low
P28482	B15ef5	mitogen-activated protein kinase	493.835	452	422.4625	456.1064	-2.25E-01	-1.28E-01	1	Unchanged Low
P20823	B09cd1	transcription factor 1; hepatic; LF	322.4762	527	423.4405	424.3654	3.93E-01	7.09E-01	1	Unchanged Low
O15250	I04cd4	X-prolyl aminopeptidase (ampho	524.8188	542	423.7387	496.7532	-3.09E-01	4.57E-02	1	Unchanged Low
P55769	P22ab8	NHP2 non-histone chromosome I	137.3557	479	424.0031	346.68	1.63E+00	1.80E+00	1	Unchanged Low
O94817	N21ab2	APG12 autophagy 12-like (S. cer	631.6055	402	424.3577	485.9574	-5.74E-01	-6.52E-01	1	Unchanged Low
O75352	K08cd5	mannose-P-dolichol utilization de	272.444	523	424.8266	406.7998	6.41E-01	9.41E-01	1	Unchanged Low
Q16585	I16cd1	sarcoglycan; beta (43kD dystrop	256.2113	293	425.1172	324.9166	7.31E-01	1.96E-01	1	Unchanged Low

Q9H7X7	B16gh5	hypothetical protein FLJ14117	261.9578	463	425.3725	383.5805	6.99E-01	8.23E-01	1	Unchanged Low
O15173	I16cd6	progesterone receptor membran	295.0481	244	425.8728	321.6602	5.29E-01	-2.74E-01	1	Unchanged Low
Q9GZQ9	A16gh4	twisted gastrulation	94.61732	147	426.1124	219.3062	2.33E+00	7.99E-01	1	Unchanged Low
Q16594	M09cd2	TAF9 RNA polymerase II; TATA	171.3507	520	426.7606	372.6331	1.32E+00	1.60E+00	1	Unchanged Low
O00479	O17gh1	high-mobility group (nonhistone)	265.695	354	426.7642	348.9168	6.84E-01	4.15E-01	1	Unchanged Low
P54760	C22ab5	EphB4	528.7065	413	427.0543	456.4179	-3.08E-01	-3.55E-01	1	Unchanged Low
P25490	F05ef6	YY1 transcription factor	481.2844	530	427.184	479.4548	-1.72E-01	1.39E-01	1	Unchanged Low
Q9JYJY	B07ef3	putative nucleolide binding prote	505.9493	431	427.3544	454.8441	-2.44E-01	-2.31E-01	1	Unchanged Low
Q09666	A22ef1	AHNAK nucleoprotein (desmoyoi	392.0671	399	427.3828	406.041	1.24E-01	2.41E-02	1	Unchanged Low
O15305	P22ab7	phosphomannomutase 2	325.0777	480	428.3778	411.2528	3.98E-01	5.63E-01	1	Unchanged Low
O60492	M09ab4	7-dehydrocholesterol reductase	388.5228	213	428.5923	343.3316	1.42E-01	-8.68E-01	1	Unchanged Low
Q9JNDS	G11cd6	nuclear pore complex interacting	280.8175	312	428.5952	340.6147	6.105E-01	1.54E-01	1	Unchanged Low
Q9HB15	M15gh5	potassium channel; subfamily K	473.5589	408	428.9306	436.9131	-1.43E-01	-2.14E-01	1	Unchanged Low
Q9Y3B4	H23ef2	CGI-110 protein	290.9669	331	429.1497	350.4806	5.61E-01	1.87E-01	1	Unchanged Low
Q14107	F05ef5	D123 gene product	387.0465	405	429.9331	407.3091	1.52E-01	6.52E-02	1	Unchanged Low
P52435	A22cd1	polymerase (RNA) II (DNA direct	527.0446	461	429.9488	472.7272	-2.94E-01	-1.93E-01	1	Unchanged Low
Q9Y262	L11ef2	eukaryotic translation initiation fa	591.5767	311	430.6788	444.385	-4.58E-01	-9.28E-01	1	Unchanged Low
P10163	L20cd2	proline-rich protein Bsn1 subfam	521.4154	251	431.1299	401.2036	-2.74E-01	-1.05E+00	1	Unchanged Low
P38378	F01cd8	protein transport protein SEC61 i	635.5838	369	431.9958	478.7225	-5.57E-01	-7.85E-01	1	Unchanged Low
P48735	B06ab6	isocitrate dehydrogenase 2 (NAC	600.2178	338	432.1616	456.8577	-4.74E-01	-8.28E-01	1	Unchanged Low
Q9NPF5	F02gh4	DNA methyltransferase 1-associat	451.5343	382	432.3473	421.964	-6.25E-02	-2.41E-01	1	Unchanged Low
O14616	K22cd4	zinc finger protein-like 1	194.5871	348	432.4885	324.9789	1.15E+00	8.38E-01	1	Unchanged Low
Q00839	A12ab7	heterogeneous nuclear ribonucleic	416.5145	410	432.5189	419.7665	5.44E-02	-2.18E-02	1	Unchanged Low
O55563	J15ef8	DKFZP564B167 protein	390.848	389	432.8082	404.2972	1.47E-01	-5.96E-03	1	Unchanged Low
Q92374	I03cd6	thorac guanine nucleotide exch	142.3392	124	433.2386	233.2947	1.61E+00	-1.95E-01	1	Unchanged Low
Q9UEE5	M07cd5	serine/threonine kinase 17a (apc	397.8599	472	433.4221	434.4129	1.24E-01	2.46E-01	1	Unchanged Low
Q9NX81	O19gh3	BTB (POZ) domain containing 2	175.3887	206	433.4811	271.6819	1.31E+00	2.33E-01	1	Unchanged Low
Q9NFX9	O01gh3	O-linked mannose beta1,2-N-acet	477.6375	353	434.2927	421.54	-1.37E-01	-4.38E-01	1	Unchanged Low
P98171	F13ef1	Rho GTPase activating protein 4	368.9887	231	435.3585	345.0241	2.39E-01	-6.77E-01	1	Unchanged Low
P56192	I14ab7	methionine-tRNA synthetase	263.0078	295	435.894	331.1505	7.29E-01	1.63E-01	1	Unchanged Low
O95411	K09cd5	TGF $\beta$ 1-induced anti-apoptotic fa	233.3926	310	436.2684	326.6136	9.025E-01	4.10E-01	1	Unchanged Low
P09132	E23cd2	signal recognition particle 19KD	227.8193	595	436.5994	419.7603	9.38E-01	1.38E+00	1	Unchanged Low
Q92537	O14gh1	KIAA0247 gene product	291.1054	232	437.1141	319.914	5.86E-01	-3.30E-01	1	Unchanged Low
P49761	G03ab4	CDC-like kinase 3	458.9266	562	437.5601	486.0405	-6.88E-02	2.91E-01	1	Unchanged Low
Q9HDC4	O19gh4	junctophilin 3	346.7829	388	439.282	391.3835	3.41E-01	1.62E-01	1	Unchanged Low
P98160	A13ef7	heparan sulfate proteoglycan 2 (0	505.6962	372	439.9544	439.0897	-2.01E-01	-4.44E-01	1	Unchanged Low
Q9NQV6	O22gh4	PR domain containing 10	369.157	514	440.5347	441.3923	2.55E-01	4.79E-01	1	Unchanged Low
Q9NRX6	J09gh4	protein x 013	324.5306	345	440.8995	370.1383	4.42E-01	8.82E-02	1	Unchanged Low
O76084	A13cd4	catenin (cadherin-associated pro	471.1305	211	441.7617	374.6479	-9.29E-02	-1.16E+00	1	Unchanged Low
P23197	E19cd7	chromobox homolog 1 (HP1 beta	480.8183	362	441.9595	428.3076	-1.22E-01	-4.09E-01	1	Unchanged Low
Q99439	E10ab6	calponin 2	429.1961	304	442.4148	391.978	4.38E-02	-4.96E-01	1	Unchanged Low
O14656	O04ef6	dystonia 1; lori (autosomal d	415.3893	533	442.9429	463.6417	-9.27E-02	3.59E-01	1	Unchanged Low
Q9NPJ3	P04gh4	uncharacterized hypothalamus p	411.0811	430	443.2575	428.1718	1.09E-01	6.55E-02	1	Unchanged Low
P41226	B10ef7	ubiquitin-activating enzyme E1-0	288.6597	342	443.334	361.2685	5.70E-01	1.95E-01	1	Unchanged Low
Q9Y478	C24cd1	protein kinase; AMP-activated; b	306.0158	165	443.5049	304.7576	5.35E-01	-8.93E-01	1	Unchanged Low
P06c8	nodal homolog (mouse)	349.4202	252	443.7188	348.2928	3.45E-01	-4.73E-01	1	Unchanged Low	
Q12904	O06ef7	small inducible cytokine subfamily	374.6683	459	445.5171	426.5346	2.50E-01	2.94E-01	1	Unchanged Low
P20264	C02cd1	POU domain; class 3; transcript	458.6994	302	447.8929	402.9521	-3.44E-02	-6.02E-01	1	Unchanged Low
Q15428	B11cd4	splicing factor 3a; subunit 2; 66k	264.0454	334	448.6652	355.7269	6.60E-01	2.36E-01	1	Unchanged Low
P49771	G06ef8	fms-related tyrosine kinase 3 lig	449.6827	417	452.1329	439.4747	7.84E-03	-1.10E-01	1	Unchanged Low
P49005	A18cd1	polymerase (DNA directed); delta	363.5225	232	452.6832	349.3417	3.16E-01	-6.49E-01	1	Unchanged Low
Q99879	M14gh6	H2B histone family; member E	325.9523	483	452.8012	420.7323	4.74E-01	5.69E-01	1	Unchanged Low
P49821	G20cd1	NADH dehydrogenase (ubiquinol	511.5488	392	454.6223	452.5721	-1.70E-01	-3.86E-01	1	Unchanged Low
P10644	H22ef5	protein kinase; cAMP-dependent	420.8225	518	454.8256	464.5909	1.12E-01	3.00E-01	1	Unchanged Low
Q9YSJ4	L17gh6	pyrimidine 5-carboxylate reductase	145.6987	303	455.1667	301.4448	1.64E+00	1.06E+00	1	Unchanged Low
P31040	K02cd2	succinate dehydrogenase complex	671.3369	351	456.2212	492.7974	-5.57E-01	-9.36E-01	1	Unchanged Low
Q9UHA2	F04ef8	synovial sarcoma translocation g	438.6951	480	456.4649	458.4094	5.73E-02	1.30E-01	1	Unchanged Low
Q9UBF6	C02ef3	ring finger protein 7	315.6541	400	456.9368	390.7196	5.34E-01	3.40E-01	1	Unchanged Low
Q9Y5S2	C21cd6	CDC42 binding protein kinase bt	386.9683	447	456.9709	430.2759	2.40E-01	2.08E-01	1	Unchanged Low
P20809	H07ef7	interleukin 11	399.048	140	458.1544	332.3748	1.99E-01	-1.51E+00	1	Unchanged Low
Q13S26	F21ef5	protein (peptidyl-prolyl cis/trans) I	333.4194	460	458.2237	417.3666	4.59E-01	4.66E-01	1	Unchanged Low
Q9NWQ9	H01gh2	hypothetical protein FLJ120671	430.7122	577	458.2293	488.6936	8.93E-02	4.22E-01	1	Unchanged Low
Q9Y6J0	E05cd8	calcineurin binding protein 1	474.3964	117	458.7489	350.127	-4.84E-02	-2.02E+00	1	Unchanged Low
Q9Y426	B13cd7	vacuolar protein sorting 45A (ye	115.1679	276	458.8586	283.3006	1.99E+00	1.26E+00	1	Unchanged Low
Q01433	G02ab2	adenosine monophosphate dea	352.5251	390	459.2935	400.6864	3.82E-01	1.47E-01	1	Unchanged Low
O43181	M07ab8	NADH dehydrogenase (ubiquinol	417.4586	432	460.2425	436.6589	1.41E-01	5.03E-02	1	Unchanged Low
Q9NWT5	D15gh5	hypothetical protein FLJ20618	354.3599	523	460.3326	445.8286	3.77E-01	5.61E-01	1	Unchanged Low
O75431	P19cd6	metaxin 2	282.4791	443	460.352	395.1258	7.05E-01	6.48E-01	1	Unchanged Low
P09543	A18gh7	2';3'-cyclic nucleotide 3' phospho	258.2662	510	462.033	409.9513	8.39E-01	9.80E-01	1	Unchanged Low
Q9BTE1	B05gh8	dynactin 4	562.6142	460	462.4054	494.9234	-2.83E-01	-2.91E-01	1	Unchanged Low
P16152	H14ab5	carbonyl reductase 1	234.3184	240	463.6916	312.5841	9.85E-01	3.30E-02	1	Unchanged Low
O15121	D06cd3	degenerative spermatocyte hom	264.7024	270	464.4612	333.1906	8.11E-01	3.08E-02	1	Unchanged Low
O60909	E09ab3	UDP-Gal:betaGlcNAc beta 1,4- c	365.8881	379	464.9697	403.197	3.46E-01	4.98E-02	1	Unchanged Low
O75223	C11gh6	hypothetical protein MGC3077	493.9011	276	465.7709	411.9427	-8.46E-02	-8.39E-01	1	Unchanged Low
Q9BQA1	K03gh8	MEP50 protein	379.1943	303	468.1997	382.8763	2.98E-01	-3.22E-01	1	Unchanged Low
O43427	F20cd4	fibroblast growth factor (acidic) lr	323.6471	325	466.8724	371.8858	5.29E-01	6.63E-03	1	Unchanged Low
Q9BWG6	A15gh6	hypothetical protein MGC3180	309.3486	596	468.0924	457.7257	5.98E-01	9.45E-01	1	Unchanged Low
Q9Y6R2	M04cd6	chromosome 4 open reading frar	337.7358	352	469.9502	386.6911	4.77E-01	6.13E-02	1	Unchanged Low
Q9HBK7	M07gh4	NPD007 protein	367.4893	469	471.1924	442.4205	3.59E-01	4.11E-01	1	Unchanged Low
P52758	E04ef7	translational inhibitor protein p14	324.9333	318	471.2741	371.3427	5.36E-01	-3.19E-02	1	Unchanged Low
P47897	E19cd1	glutaminyl-tRNA synthetase	400.1718	364	472.5359	412.2837	2.40E-01	-1.36E-01	1	Unchanged Low
Q9BWQ6	P20gh5	hypothetical protein MGC3262	288.8083	483	473.0084	415.0843	7.12E-01	7.43E-01	1	Unchanged Low
P35325	H22cd2	small proline-rich protein 2B	390.5307	584	474.2762	483.0992	2.80E-01	5.82E-01	1	Unchanged Low
Q9HA68	O23gh5	hypothetical protein FLJ12154	556.3676	383	474.593	471.3877	-2.29E-01	-5.38E-01	1	Unchanged Low
P49366	P16ab5	deoxyhypusine synthase	458.6886	481	477.1999	472.2313	5.71E-02	6.79E-02	1	Unchanged Low
Q9UKZ7	J18ef1	colon carcinoma related protein	505.0162	450	478.4767	477.7496	-7.79E-02	-1.67E-01	1	Unchanged Low

P01730	K15ef5	CD4 antigen (p55)	516.4046	432	478.8033	475.788	-1.09E-01	-2.57E-01	1	Unchanged	Low
P20674	L06cd4	cytochrome c oxidase subunit Va	512.4055	372	480.2708	454.7764	-9.34E-02	-4.63E-01	1	Unchanged	Low
Q12828	H02ef6	far upstream element (FUSE) b1n	462.592	312	480.3079	418.2668	5.48E-02	-5.69E-01	1	Unchanged	Low
Q9Y6A4	J18ef3	similar to mouse Gl3 or D. malar	359.9248	485	480.6661	442.0882	4.18E-01	4.32E-01	1	Unchanged	Low
O60888	B09ef2	divalent cation tolerant protein C	298.6981	304	481.1138	361.3342	6.88E-01	2.62E-02	1	Unchanged	Low
O75716	F08cd3	serine/threonine kinase 16	384.1875	373	481.1652	408.0382	4.02E-01	5.68E-02	1	Unchanged	Low
P30711	E18ef7	glutathione S-transferase theta 1	327.8121	533	481.9461	447.6268	5.56E-01	7.02E-01	1	Unchanged	Low
Q15008	L03gh1	KIAA0107 gene product	475.6485	506	482.3327	488.0851	2.01E-02	9.00E-02	1	Unchanged	Low
P17174	N07ab4	glutamic-oxaloacetic transaminat	412.5293	224	484.4384	373.5229	2.32E-01	-8.84E-01	1	Unchanged	Low
P13798	K16ab2	N-acylaminoacyl-peptide hydrol	365.1218	351	484.44	400.3314	4.08E-01	-5.51E-02	1	Unchanged	Low
Q9P2R8	E15ef4	Missshapen/NIK-related kinase	469.5725	511	484.515	488.4865	4.52E-01	1.23E-01	1	Unchanged	Low
Q9UNT1	E20cd7	RAB; member of RAS oncogene	268.9116	347	484.9919	366.9843	8.51E-01	3.68E-01	1	Unchanged	Low
O75607	L11cd7	nucleophosmin/nucleoplasmin; 3	350.2387	272	485.5671	369.1972	4.71E-01	-3.66E-01	1	Unchanged	Low
O94925	B20gh1	glutaminase	410.4357	471	486.8946	456.0458	2.46E-01	1.98E-01	1	Unchanged	Low
O95390	A06ab3	growth differentiation factor 11	264.606	324	488.3912	359.3416	8.87E-01	2.92E-01	1	Unchanged	Low
O75956	K13cd6	tumor suppressor deleted In oral	524.962	482	489.6212	498.9664	-1.01E-01	-1.22E-01	1	Unchanged	Low
O95573	I23ab5	fatty-acid-Coenzyme A ligase; iso	345.1387	174	489.6455	339.2885	4.67E-01	-1.02E+00	1	Unchanged	Low
Q9BXH1	N23gh6	Bcl-2 binding component 3	493.3887	433	492.1063	472.8963	-3.75E-03	-1.88E-01	1	Unchanged	Low
P13662	L20cd5	nuclear transport factor 2	392.576	479	492.4942	454.7336	3.27E-01	2.87E-01	1	Unchanged	Low
Q92793	H05ab5	CREB binding protein (Rubinstel	468.559	474	494.3525	478.8243	7.73E-02	1.53E-02	1	Unchanged	Low
Q9P0H6	K23ef4	AD-012 protein	406.4789	469	495.1858	456.7944	2.85E-01	2.06E-01	1	Unchanged	Low
Q9P0R3	C05ef3	hypothetical protein HSPC213	339.0916	509	495.2656	447.9021	5.47E-01	5.87E-01	1	Unchanged	Low
O75094	E11gh1	sil homolog 3 (Drosophila)	345.9855	439	496.3612	426.952	5.21E-01	3.42E-01	1	Unchanged	Low
Q9P011	P10ef2	non-canonical ubiquitin conjugati	480.4398	538	497.256	498.5084	1.11E-01	2.24E-01	1	Unchanged	Low
Q92504	M12cd4	HLA class II region expressed ge	251.7256	339	497.6138	362.6669	9.83E-01	4.28E-01	1	Unchanged	Low
O95190	L12cd8	omithine decarboxylase antizym	421.0592	441	497.6839	453.1247	2.41E-01	6.55E-02	1	Unchanged	Low
Q9Y230	N12cd6	RuvB-like 2 (E. coli)	342.0841	300	497.7767	379.9805	5.41E-01	-1.89E-01	1	Unchanged	Low
Q9BSG0	M16gh8	chromosome 2 open reading frar	342.5321	458	497.8462	426.9191	6.17E-01	4.98E-01	1	Unchanged	Low
Q9Y366	I17ef2	chromosome 20 open reading frar	278.1968	453	498.3057	409.8539	8.41E-01	7.04E-01	1	Unchanged	Low
Q14094	O24ef5	cyclin I	407.6242	354	499.6223	420.31	2.94E-01	-2.05E-01	1	Unchanged	Low
P43403	H04ef5	zeta-chain (TCR) associated pro	396.0583	396	500.6282	430.7684	3.38E-01	-1.60E-03	1	Unchanged	Low
P52803	H23ef7	ephrinA5	357.5339	316	501.0718	391.4643	4.87E-01	-1.79E-01	1	Unchanged	Low
O95402	E18cd5	cofactor required for Sp1 transci	106.0683	587	501.9814	222.265	2.24E+00	-8.52E-01	1	Unchanged	Low
O00233	L23ab8	proteasome (prosome; macropah	581.8818	399	502.2028	494.287	-2.12E-01	-5.45E-01	1	Unchanged	Low
Q9H1K6	O18gh7	mesoderm development candida	432.735	560	502.7516	498.6205	2.16E-01	3.73E-01	1	Unchanged	Low
Q9BXL6	K15gh6	caspase recruitment domain prot	425.1251	523	502.8514	483.6229	2.42E-01	2.99E-01	1	Unchanged	Low
Q9H173	H03gh5	endoplasmic reticulum chaperon	456.5646	449	503.5156	469.6418	1.41E-01	-2.46E-02	1	Unchanged	Low
Q9NV83	H03gh3	hypothetical protein FLJ10876	423.9423	497	504.9702	475.4325	2.52E-01	2.30E-01	1	Unchanged	Low
P11926	A12ab8	omithine decarboxylase 1	591.3922	362	505.3016	486.3355	-2.27E-01	-7.07E-01	1	Unchanged	Low
Q40743	D23ef1	empty spiracles homolog 2 (Dros	531.3866	311	505.7367	449.3322	-7.14E-02	-7.73E-01	1	Unchanged	Low
Q9BVK2	G11gh6	hypothetical protein MGC2840 s	388.8682	383	505.9804	425.9595	3.80E-01	-2.16E-02	1	Unchanged	Low
O43251	I16ef3	RNA binding motif protein 9	346.6445	530	507.0674	481.1452	5.49E-01	6.12E-01	1	Unchanged	Low
Q99829	L13cd4	copine I	355.3783	268	508.4915	377.1688	5.17E-01	-4.09E-01	1	Unchanged	Low
O95769	I21ef2	U6 snRNA-associated Sm-like pr	391.981	311	508.6863	403.8163	3.77E-01	-3.36E-01	1	Unchanged	Low
Q9UN53	C19ef2	calcium binding protein Cab45 p	327.721	407	509.3318	414.6963	6.36E-01	3.13E-01	1	Unchanged	Low
P24310	F03ab4	cytochrome c oxidase subunit VII	184.0695	288	509.4504	327.1972	1.47E+00	6.46E-01	1	Unchanged	Low
Q9H929	N09gh5	hypothetical protein FLJ13055	387.341	500	510.1197	465.7217	3.97E-01	3.67E-01	1	Unchanged	Low
P10768	K19ef1	esterase D-formylglutathione hyd	596.3068	102	510.5002	402.8142	-2.24E-01	-2.55E+00	1	Unchanged	Low
O95287	D17cd5	golgi autoantigen; golgin subfam	465.1135	560	510.6433	472.3714	5.61E-01	6.95E-01	1	Unchanged	Low
Q11015	H16cd1	SET translocation (myeloid leuke	328.6513	403	511.1477	414.2142	6.37E-01	2.94E-01	1	Unchanged	Low
Q9UK45	B08ef2	U6 snRNA-associated Sm-like pr	388.4486	551	511.9386	483.7088	3.98E-01	5.04E-01	1	Unchanged	Low
P35611	I17ab2	adducin 1 (alpha)	435.0349	519	512.6447	488.7819	2.37E-01	2.54E-01	1	Unchanged	Low
O14681	K22cd5	eloposide-induced mRNA	451.5599	324	516.5292	430.8211	1.94E-01	-4.77E-01	1	Unchanged	Low
P80303	A05cd1	nucleobindin 2	296.1418	236	516.7037	349.5918	8.03E-01	-3.28E-01	1	Unchanged	Low
Q9NW0C	N19gh2	F-box only protein 4	434.5394	477	517.7728	476.3476	2.53E-01	1.34E-01	1	Unchanged	Low
P00367	B06ab5	glutamate dehydrogenase 1	360.6	303	518.2525	394.0342	5.23E-01	-2.50E-01	1	Unchanged	Low
O00469	I09ab8	procollagen-lysine; 2-oxoglutar	735.8327	238	518.6446	497.4006	-5.05E-01	-1.63E-00	1	Unchanged	Low
Q9U040	M18ef4	mitochondrial ribosomal protein L	364.1383	336	520.3777	406.7523	5.15E-01	-1.17E-01	1	Unchanged	Low
P20338	N08ab8	RAB4A; member RAS oncogene	487.9427	457	520.7608	488.5317	9.39E-02	-9.49E-02	1	Unchanged	Low
Q9HCU8	I19gh4	polymerase (DNA-directed); delta	513.52	431	522.5153	489.0161	2.51E-02	-2.53E-01	1	Unchanged	Low
P00519	I06ef5	v-abl Abelson murine leukem	323.4636	301	522.7624	352.0574	1.17E+00	3.73E-01	1	Unchanged	Low
Q13880	O02cd5	brain and reproductive organ-exq	572.4849	263	523.9906	453.0588	-1.28E-01	-1.12E+00	1	Unchanged	Low
P25789	L13ef7	proteasome (prosome; macroph	436.5895	534	526.397	498.9408	2.70E-01	2.90E-01	1	Unchanged	Low
O43805	J16cd3	Sjogren's syndrome nuclear auto	368.0123	539	526.5215	477.7167	5.17E-01	5.50E-01	1	Unchanged	Low
O75817	A13cd6	POP7 (processing of precursor; t	375.1187	433	526.6432	445.0255	4.89E-01	2.08E-01	1	Unchanged	Low
Q9UB11	N11cd7	BUP protein	337.1018	428	526.9646	430.701	6.45E-01	3.45E-01	1	Unchanged	Low
P03950	G12ab2	angiogenin; ribonuclease; RNase	395.0198	200	527.7882	374.4251	4.18E-01	-9.79E-01	1	Unchanged	Low
P78423	F20cd1	small inducible cytokine subfam	201.965	747	530.2357	493.2272	1.39E+00	1.89E+00	1	Unchanged	Low
Q9P1D0	E07gh4	hypothetical protein PRO2533	58.04051	73.3	531.5331	220.9467	3.20E+00	3.36E-01	1	Unchanged	Low
P03999	K05ab3	opsin 1 (cone pigments); short-w	116.5093	37.9	532.8048	229.0788	2.19E+00	-1.62E+00	1	Unchanged	Low
O95793	M22cd5	staufen; RNA binding protein (Dr	417.7687	498	534.8626	483.6536	3.56E-01	2.54E-01	1	Unchanged	Low
P22750	M05ef2	RAB4B; member RAS oncogene	297.3584	346	536.4865	393.9782	8.57E-01	2.19E-01	1	Unchanged	Low
B06gh8	B06gh8	ubiquitin UBF-II	431.0731	472	540.8482	481.1517	3.27E-01	1.29E-01	1	Unchanged	Low
Q9NRX8	J15gh4	oxidoreductase UCPA	168.7047	523	544.0864	411.9671	1.69E+00	1.63E+00	1	Unchanged	Low
Q9UHQ3	J20gh4	stromal cell protein	469.8784	214	546.1893	410.1503	2.17E-01	-1.13E+00	1	Unchanged	Low
Q96552	J22gh8	phosphatidylinositol glycan; clas	404.9498	287	548.8908	412.8095	4.34E-01	-4.99E-01	1	Unchanged	Low
Q9H3F6	C24gh8	MSTP028 protein	442.9007	398	549.0707	462.5636	3.10E-01	-1.63E-01	1	Unchanged	Low
P37198	K03cd8	nudeoporin 62kD	428.2961	499	550.8083	492.7531	3.63E-01	2.21E-01	1	Unchanged	Low
Q9H1D4	B05gh4	arginyl aminopeptidase (aminope	430.3273	477	551.8541	486.2744	3.59E-01	1.47E-01	1	Unchanged	Low
O75350	K04cd5	glycoprotein; synaptic	480.7082	436	552.8489	489.9278	2.02E-01	-1.40E-01	1	Unchanged	Low
Q9P024	D16ef3	Huntingtin interacting protein K	369.5132	480	553.5493	467.714	5.83E-01	3.78E-01	1	Unchanged	Low
Q9Y224	H21ef2	CG1-99 protein	449.089	472	554.6607	492.0453	3.05E-01	7.30E-02	1	Unchanged	Low
Q13361	O12cd3	Microfibril-associated glycoprotein	194.28	354	557.066	368.553	1.52E+00	8.67E-01	1	Unchanged	Low
Q02535	F01ef1	Inhibitor of DNA binding 3; domir	84.05787	174	559.513	272.6788	2.73E+00	1.05E+00	1	Unchanged	Low
O95864	L24cd4	fatty acid desaturase 2	298.4502	113	559.6571	323.8122	9.07E-01	-1.40E+00	1	Unchanged	Low
P53621	H16ab4	coatomer protein complex; subar	409.2779								

P35638	N03ab4	DNA-damage-inducible transcript	322.5942	318	565.361	401.9484	8.09E-01	-2.12E-02	1	Unchanged Low
P22307	D22cd1	sterol carrier protein 2	354.3674	358	569.1558	426.421	6.84E-01	5.58E-03	1	Unchanged Low
Q92543	D15gh1	KIAA0254 gene product	328.3511	356	569.5472	417.8592	7.95E-01	1.15E-01	1	Unchanged Low
P78330	N06ab8	phosphoserine phosphatase	253.4253	220	569.9825	347.8406	1.17E+00	-2.03E-01	1	Unchanged Low
Q9UNX3	G15ef2	ribosomal protein L26-like 1	401.3697	445	572.3441	472.8205	5.12E-01	1.48E-01	1	Unchanged Low
P49189	C10ab2	aldehyde dehydrogenase 9 family	446.252	277	579.314	434.2707	3.76E-01	-8.87E-01	1	Unchanged Low
Q9ULX0	H03gh8	Inorganic pyrophosphatase	488.3446	402	579.6142	489.9828	2.47E-01	-2.81E-01	1	Unchanged Low
O15353	H21cd3	winged-helix nude	407.9375	497	580.6191	495.2368	5.09E-01	2.85E-01	1	Unchanged Low
Q9NRP2	D21gh4	DC13 protein	382.8544	421	581.5421	461.731	6.03E-01	1.36E-01	1	Unchanged Low
Q16280	E18ef1	cyclic nucleotide gated channel	464.0608	360	584.8035	469.8748	3.34E-01	-3.66E-01	1	Unchanged Low
P04183	C04cd2	thymidine kinase 1; soluble	346.7317	289	588.3101	407.8979	7.63E-01	-2.64E-01	1	Unchanged Low
Q12824	O17ef5	SWI/SNF related; matrix associ	218.8831	554	590.2326	454.3734	1.43E+00	1.34E+00	1	Unchanged Low
Q99719	B09ab8	peanut-like 1 (Drosophila)	419.5269	410	592.2598	474.0479	4.97E-01	-3.19E-02	1	Unchanged Low
P46100	H07ab3	alpha thalassemia/mental retard	309.8648	167	594.3041	356.9983	9.40E-01	-6.93E-01	1	Unchanged Low
Q16610	O05ab5	extracellular matrix protein 1	238.3172	335	596.1691	389.6774	1.32E+00	4.89E-01	1	Unchanged Low
P39656	E23ab6	dolichyl-diphosphooligosaccharide	433.6719	367	598.0668	468.4028	4.84E-01	-2.39E-01	1	Unchanged Low
P53814	G07cd3	smoathelin	517.4102	269	598.16	461.5158	2.09E-01	-9.44E-01	1	Unchanged Low
Q9PQ4	P24ef1	hypothetical protein LOC51260	609.9142	288	601.9324	499.2558	-1.90E-02	-1.09E+00	1	Unchanged Low
Q9BX21	A02gh7	peptidyl prolyl isomerase (cyclo-	465.4301	362	603.8737	477.1895	3.76E-01	-3.62E-01	1	Unchanged Low
Q9Y204	H19ef8	HSPC002 protein	337.5615	391	604.9187	444.641	8.42E-01	2.14E-01	1	Unchanged Low
O15527	A18ab8	8-oxoguanine DNA glycosylase	330.4852	282	605.3444	406.0683	8.73E-01	-2.27E-01	1	Unchanged Low
Q04323	G01ef2	ORF	497.159	255	610.1121	454.2076	2.95E-01	-9.61E-01	1	Unchanged Low
P20204	G18ab4	proliferating cell nuclear antigen	332.1465	303	612.821	416.0883	8.84E-01	-1.31E-01	1	Unchanged Low
Q99720	M11cd6	sigma receptor (SR31747) binding	363.8609	379	615.0729	452.6168	7.57E-01	5.85E-02	1	Unchanged Low
P43307	G13cd2	signal sequence receptor; alpha	226.1566	322	618.5394	389.0352	1.45E+00	5.10E-01	1	Unchanged Low
Q9H378	O05gh5	chromosome 20 open reading fr	221.2984	246	619.4944	362.4108	1.49E+00	1.55E-01	1	Unchanged Low
Q9RNX2	A08gh5	mitochondrial ribosomal protein l	284.6282	305	627.9834	405.9846	1.14E+00	1.01E-01	1	Unchanged Low
Q9P2X0	L10gh2	dolichyl-phosphate mannosyltran	285.542	431	638.6695	451.8107	1.16E+00	5.95E-01	1	Unchanged Low
Q9Y5Z8	E05cd7	male-specific lethal 3-like 1 (Dro	361.7331	394	639.7431	465.0297	8.23E-01	1.22E-01	1	Unchanged Low
P78524	F01cd2	suppression of tumorigenicity 5	343.4117	289	643.333	425.1425	9.06E-01	-2.50E-01	1	Unchanged Low
P55145	F02ab2	arginine-rich; mutated in early st	413.1582	420	656.6324	498.4892	6.68E-01	2.26E-02	1	Unchanged Low
P33551	O23ab5	CDC28 protein kinase 1	296.3533	355	671.4891	440.861	1.18E+00	2.59E-01	1	Unchanged Low
Q9BVQ0	E09gh6	hypothetical protein MGC5363	43.30768	54.5	681.2449	259.6855	3.98E-01	3.32E-01	1	Unchanged Low
P34897	D15cd2	serine hydroxymethyltransferase	440.9652	290	686.5584	472.1838	6.37E-01	-6.05E-01	1	Unchanged Low
Q9Y5B4	L23ef2	androgen induced protein	268.4081	519	685.9395	491.1814	1.35E+00	9.52E-01	1	Unchanged Low
Q9Y2V5	B15ef2	transforming growth factor beta 1	249.1479	327	712.3879	429.636	1.52E+00	3.94E-01	1	Unchanged Low
Q13953	B19cd2	solute carrier family 12 (polassi)	342.5865	428	729.2688	499.9658	1.09E+00	3.21E-01	1	Unchanged Low
Q92686	I11ef6	neurogranin (protein kinase C su	330.8792	299	736.2348	455.4495	1.15E+00	-1.45E-01	1	Unchanged Low
O60656	J05cd8	cysteine knot superfamily 1; BMF	106.6904	151	781.0154	346.3594	2.87E+00	5.05E-01	1	Unchanged Low
Q9Y4M4	I21gh3	putative UDP-GalNAc polypeptid	346.098	251	846.4309	481.2315	1.29E+00	-4.63E-01	1	Unchanged Low
P16581	E01ef7	selectin E (endothelial adhesion	109.3094	378	875.1666	454.0605	3.00E+00	1.79E+00	1	Unchanged Low
O14733	P02ef5	mitogen-activated protein kinase	98.83312	140	888.014	375.5944	3.17E+00	5.02E-01	1	Unchanged Low
Q16523	M24cd2	synaptin 1A (brain)	403.2337	165	926.5022	498.3425	1.20E+00	-1.29E+00	1	Unchanged Low
Q9P1M5	P12gh3	WW domain containing oxidored	38.93	19.3	129.23	450.1426	5.05E+00	-1.01E+00	1	Unchanged Low
O60613	L18cd4	15 kDa selenoprotein	1220.802	1110	1285.07	1205.045	7.38E-02	-1.38E-01	2	Unchanged Medium
Q16698	M07ab4	2,4-dienoyl CoA reductase 1; mit	469.9997	706	615.3087	597.2594	3.89E-01	5.88E-01	2	Unchanged Medium
Q9HBA8	D23gh1	24-dehydrocholesterol reductase	768.0888	278	626.0195	557.2677	-2.95E-01	-1.47E+00	2	Unchanged Medium
Q9P012	M13ef4	30 kDa protein	546.352	691	644.5795	617.4113	1.70E-01	3.39E-01	2	Unchanged Medium
Q9UL53	P24cd7	5'-3' exonuclease 2	648.132	604	430.2235	560.6322	-5.91E-01	-1.03E-01	2	Unchanged Medium
P49902	N16cd7	5'-nucleotidase; cytosolic II	1040.523	1220	440.0817	900.9404	-1.24E+00	2.32E-01	2	Unchanged Medium
Q95336	P09cd7	6-phosphogluconolactonase	524.3104	755	812.5595	697.4428	6.32E-01	5.27E-01	2	Unchanged Medium
Q03393	A23ab8	6-pyruvoyltetrahydropterin synth	358.0591	700	517.4355	525.0184	5.31E-01	9.66E-01	2	Unchanged Medium
Q13443	P01ef7	a disintegrin and metalloprotein	1306.754	481	445.3663	744.5037	-1.55E+00	-1.44E+00	2	Unchanged Medium
O75173	F15ab2	a disintegrin-like and metalloprotein	766.5151	1060	1254.604	1033.448	6.74E-01	4.29E-01	2	Unchanged Medium
P51572	O03gh1	accessory protein SAP31/BAP2	985.1381	889	656.6554	843.6943	-5.85E-01	-1.48E-01	2	Unchanged Medium
P42765	D03ab2	acetyl-Coenzyme A acyltransfera	849.6041	1280	1204.131	1113.329	5.03E-01	5.92E-01	2	Unchanged Medium
P24666	E05ab2	acid phosphatase 1; soluble	1642.966	1970	1890.903	1833.204	2.03E-01	2.59E-01	2	Unchanged Medium
Q92688	D21cd6	acdc (leucine-rich) nuclear phar	470.8575	289	813.9103	531.9498	8.28E-01	-7.04E-01	2	Unchanged Medium
O14539	B21ab2	actin binding LIM protein	1351.973	393	358.779	701.2899	-1.91E+00	-1.78E+00	2	Unchanged Medium
O15143	F06ab2	actin related protein 2/3 complex	696.0033	513	349.0474	519.3549	-9.96E-01	-4.40E-01	2	Unchanged Medium
O15609	F12ab2	actin related protein 2/3 complex	909.0832	889	807.751	868.6913	-1.71E-01	-3.18E-02	2	Unchanged Medium
O15511	F14ab2	actin related protein 2/3 complex	732.1996	619	466.1372	605.8842	-6.51E-01	-2.42E-01	2	Unchanged Medium
P21278	A08ab6	actin; gamma 2; smooth muscle	585.3438	846	2095.96	1175.856	1.84E+00	5.32E-01	2	Unchanged Medium
Q9P016	O09ef4	AD-015 protein	947.0366	837	1259.571	1014.448	4.11E-01	-1.79E-01	2	Unchanged Medium
O43747	M13ab2	adaptor-related protein complex	1104.332	532	419.4712	685.2957	-1.40E+00	-1.05E+00	2	Unchanged Medium
P20172	A11ab6	adaptor-related protein complex	1286.83	1280	2285.193	1617.354	8.29E-01	-7.63E-03	2	Unchanged Medium
O14617	H07ab2	adaptor-related protein complex	679.4847	495	357.0868	510.4994	-9.28E-01	-4.57E-01	2	Unchanged Medium
P07741	M24ab2	adenine phosphoribosyltransfera	1885.065	862	823.8455	1190.468	-1.19E+00	-1.13E+00	2	Unchanged Medium
P00568	A02ab2	adenylyl kinase 1	2404.119	399	354.3764	1052.361	-2.76E+00	-2.59E+00	2	Unchanged Medium
Q9UJ7	I06ef2	adenylyl kinase 3 alpha like	758.7288	1060	662.8834	828.3993	-1.95E-01	4.87E-01	2	Unchanged Medium
P30566	M07ab2	adenylosuccinate lyase	495.8874	622	518.4238	545.4304	6.41E-02	3.27E-01	2	Unchanged Medium
Q16186	M11cd7	adhesion regulating molecule 1	622.3901	610	574.5888	602.2578	-1.15E-01	-2.95E-02	2	Unchanged Medium
Q9NVF6	B19gh3	ADP-ribosylation factor 1 GTPas	449.3679	623	676.1678	582.9297	5.90E-01	4.72E-01	2	Unchanged Medium
P26438	B04ab2	ADP-ribosylation factor 6	732.1241	818	876.9277	809.1342	2.60E-01	1.61E-01	2	Unchanged Medium
P46016	D12ab2	ADP-ribosylation factor-like 1	827.1898	1220	1141.92	1064.016	4.65E-01	5.64E-01	2	Unchanged Medium
P36404	D14ab2	ADP-ribosylation factor-like 2	1751.048	1550	1871.661	1723.74	9.61E-01	-1.77E-01	2	Unchanged Medium
P56559	D20ab2	ADP-ribosylation factor-like 7	485.4562	598	568.6824	550.5764	2.28E-01	3.00E-01	2	Unchanged Medium
P35368	K17ab2	adrenergic; alpha-1B; receptor	1433.715	1510	1335.995	1426.069	-1.02E-01	7.34E-02	2	Unchanged Medium
P15144	G24ab2	alanyl (membrane) aminopeptida	987.3343	222	480.1162	563.2289	-1.04E+00	-2.15E+00	2	Unchanged Medium
P30038	L09ab2	aldehyde dehydrogenase 4 famili	1178.797	598	657.4315	811.7082	-8.44E-01	-9.81E-01	2	Unchanged Medium
P14550	L05ab2	aldo-keto reductase family 1; mei	555.464	888	609.9901	683.9189	1.35E+01	6.74E-01	2	Unchanged Medium
O43488	L07ab2	aldo-keto reductase family 7; mei	546.409	525	748.5424	606.6855	4.54E-01	-5.74E-02	2	Unchanged Medium
P09972	C16ab2	aldolase C; fructose-bisphosphat	878.5714	1050	947.5062	960.156	1.09E-01	2.63E-01	2	Unchanged Medium
O43590	G12ef4	alpha-acidin-2-associated LIM p	776.3757	1070	501.1993	783.883	-6.31E-01	4.68E-01	2	Unchanged Medium
Q08117	M19ab2	amino-terminal enhancer of split	1779.707	1430	1219.695	1476.318	-5.45E-01	-3.16E-01	2	Unchanged Medium
Q13438	G05cd7	amplified in osteosarcoma	658.0513	638	802.3407	699.6136	2.86E-01	-4.36E-02	2	Unchanged Medium

O96018	M01gh1	amyloid beta (A4) precursor prot	762.3898	750	1117.682	876.6611	5.52E-01	-2.38E-02	2 Unchanged Medium
Q13564	P11ab2	amyloid beta precursor protein bl	587.5144	664	786.6426	679.5497	4.21E-01	1.78E-01	2 Unchanged Medium
Q9Y679	B08cd7	ancient ubiquitous protein 1	1191.741	1270	1022.771	1160.442	-2.21E-01	8.81E-02	2 Unchanged Medium
Q9UKB4	B12ef2	angiomotin like 2	523.7253	776	568.8766	622.7291	1.19E-01	5.66E-01	2 Unchanged Medium
Q13725	H19ab2	angiotensin receptor 1	1495.332	1360	1058.942	1304.886	-4.98E-01	-1.36E-01	2 Unchanged Medium
P08133	I20ab2	annexin A6	253.0936	413	879.9474	515.5041	1.80E+00	7.08E-01	2 Unchanged Medium
P20073	I22ab2	annexin A7	650.1591	481	420.4945	517.0979	-6.29E-01	-4.36E-01	2 Unchanged Medium
P03971	E22ab2	anti-Müllerian hormone	1140.812	948	640.7158	809.9247	-6.32E-01	-2.67E-01	2 Unchanged Medium
P30041	O08cd5	anti-oxidant protein 2 (non-selen)	1248.922	1160	3067.945	1824.225	1.30E+00	-1.12E-01	2 Unchanged Medium
P27695	K06ef1	APEX nuclease (multi-functional)	665.9854	653	835.6897	718.2149	3.27E-01	-2.85E-02	2 Unchanged Medium
Q9Y4J7	P01ab2	apoptosis inhibitor 5	1850.534	68.4	147.4186	688.7802	-3.65E+00	-4.76E+00	2 Unchanged Medium
Q9Y5L7	L03ef2	apoptosis related protein APR-3	662.9122	583	1426.469	890.7729	1.11E+00	-1.86E-01	2 Unchanged Medium
Q94778	O14ab2	aquaporin 8	1475.036	1420	1474.307	1455.01	-7.13E-04	-5.92E-02	2 Unchanged Medium
O15296	E02ab2	arachidonate 15-lipoxygenase; s-	826.8209	607	720.2105	718.1334	-1.99E-01	-4.45E-01	2 Unchanged Medium
P48444	O18ab2	archain 1	1291.871	1200	1374.223	1288.649	8.92E-02	-1.07E-01	2 Unchanged Medium
P00968	J24ab2	argininosuccinate synthetase	1049.688	1600	949.4889	1199.548	-1.45E-01	6.08E-01	2 Unchanged Medium
P42024	D15ab2	ARP1 actin-related protein 1 hom	1054.266	1720	1777.944	1518.804	7.54E-01	7.10E-01	2 Unchanged Medium
O43681	J16ab2	arsA arsenite transporter; ATP-bl	540.3448	724	595.3348	620.0089	1.40E-01	4.23E-01	2 Unchanged Medium
Q9ULX3	E02el4	ART-4 protein	728.7274	595	509.3934	611.0757	-5.17E-01	-2.92E-01	2 Unchanged Medium
O96030	H16ab2	artemin	881.7849	728	638.2016	749.363	-4.66E-01	-2.76E-01	2 Unchanged Medium
P15289	F24ab2	arylsulfatase A	1639.546	1230	1012.121	1294.172	-6.96E-01	-4.14E-01	2 Unchanged Medium
P08243	J18ab2	asparagine synthetase	891.3027	643	1540.113	1024.719	7.89E-01	-4.72E-01	2 Unchanged Medium
O95630	L17ab2	associated molecule with the SH <sup>+</sup>	660.3522	872	729.2363	753.7548	1.43E-01	4.01E-01	2 Unchanged Medium
O95135	B09ab2	ataxin 2 related protein	902.4529	345	342.3299	530.0852	-1.40E+00	-1.39E+00	2 Unchanged Medium
O14530	N15ab2	ATP binding protein associated w	827.4646	1390	766.257	993.482	-1.11E-01	7.45E-01	2 Unchanged Medium
P30049	N20ab2	ATP synthase; H <sup>+</sup> transporting; r	625.0408	468	441.4691	511.6658	-5.02E-01	-4.16E-01	2 Unchanged Medium
Q9UI12	H0ef2	ATPase inhibitor precursor	776.4612	1220	641.2767	878.5341	-2.76E-01	6.49E-01	2 Unchanged Medium
Q9Y5K8	F17ef2	ATPase; H <sup>+</sup> transporting; lysoso	998.0597	1670	1029.886	1232.91	4.53E-02	7.43E-01	2 Unchanged Medium
Q75787	P15ab2	ATPase; H <sup>+</sup> transporting; lysoso	815.707	945	1081.688	947.5842	4.07E-01	2.13E-01	2 Unchanged Medium
P05023	P09ef5	ATPase; Na <sup>+</sup> /K <sup>+</sup> transporting; alj	1299.236	517	709.0882	841.8422	-8.74E-01	-1.33E+00	2 Unchanged Medium
P45844	P13ef5	ATP-binding cassette; sub-family	863.8068	381	606.1642	616.8957	-5.11E-01	-1.18E+00	2 Unchanged Medium
Q9HAP7	M08gh5	baculoviral IAP repeat-containing	1507.175	1740	1945.196	1730.54	3.68E-01	2.07E-01	2 Unchanged Medium
Q94812	G09ab3	BA11-associated protein 3	1073.67	983	826.6524	961.2437	-3.77E-01	-1.27E-01	2 Unchanged Medium
P35613	B14ef7	basigin (OK blood group)	603.4821	474	865.2409	647.414	5.20E-01	-3.50E-01	2 Unchanged Medium
Q9BSRG	A20gh8	BBP-like protein 1	816.219	1320	914.1927	1015.173	1.64E-01	6.88E-01	2 Unchanged Medium
O00512	K01ab3	B-cell CLL/lymphoma 9	1357.15	767	80.36541	504.741	-4.08E+00	-4.15E+00	2 Unchanged Medium
Q12983	E19ab5	BCL2-adenovirus E1B 19kD Intel	763.7046	548	991.4529	767.5569	3.77E-01	-4.80E-01	2 Unchanged Medium
Q92934	K24ef1	BCL2-antagonist of cell death	538.8191	727	603.5103	623.2249	1.64E-01	4.33E-01	2 Unchanged Medium
Q7817	E10ef6	BCL2-like 1	2062.673	2510	1097.372	1890.905	-9.10E-01	2.85E-01	2 Unchanged Medium
O43892	M23ab3	Bicaudal D homolog 1 (Drosophila)	654.9397	414	548.7409	539.1375	-2.55E-01	-6.63E-01	2 Unchanged Medium
P53004	O19ab3	biliverdin reductase A	490.0724	569	512.2807	523.696	6.39E-02	2.15E-01	2 Unchanged Medium
O60629	G21ab3	bladder cancer associated prote	607.9847	1180	1083.411	956.1289	8.33E-01	9.53E-01	2 Unchanged Medium
Q9HBX3	N21gh5	brain and nasopharyngeal carcin	1672.876	544	44.02679	590.2997	-5.25E+00	-4.95E+00	2 Unchanged Medium
P56945	H23ef3	breast cancer anti-estrogen resis	1334.88	1300	1304.356	1312.13	-3.34E-02	-4.14E-02	2 Unchanged Medium
O15255	G21cd6	CAAX box 1	733.6878	577	1202.182	837.48	7.12E-01	-3.48E-01	2 Unchanged Medium
P12830	C16ef5	cadherin 1; type 1; E-cadherin (e	1094.64	924	489.5012	835.8959	-1.16E+00	-2.45E-01	2 Unchanged Medium
P19022	E03ef7	cadherin 2; type 1; N-cadherin (n	337.5528	540	747.1198	541.7151	1.15E+00	6.79E-01	2 Unchanged Medium
P22223	K19ef7	cadherin 3; type 1; P-cadherin (p	896.8467	1200	372.3054	823.6929	-1.27E+00	-4.22E-01	2 Unchanged Medium
P22676	N07ab5	calbindin 2; (29kD; calretinin)	1781.134	1500	2116.438	1797.589	2.49E-01	-2.52E-01	2 Unchanged Medium
Q99828	O19gh1	calcium and integrin binding 1 (c	1130.551	1320	836.3709	1096.979	-4.31E-01	2.26E-01	2 Unchanged Medium
P02593	H18ab4	calmodulin 1 (phosphorylase klin	1076.299	787	983.6302	949.1389	-1.30E-01	-5.51E-01	2 Unchanged Medium
Q13942	L01ab5	calmodulin 3 (phosphorylase klin	902.667	464	871.1455	746.0174	-5.13E-02	-9.59E-01	2 Unchanged Medium
P27824	J05ef1	calnexin	1492.644	1370	1543.709	1470.4	4.85E-02	-1.19E-01	2 Unchanged Medium
P17655	C20ef6	calpain 2; (mVII) large subunit	671.5939	837	549.4365	685.847	-2.90E-01	3.17E-01	2 Unchanged Medium
P04632	C22ef6	calpain; small subunit 1	1565.935	1650	1258.047	1490.643	-3.16E-01	7.36E-02	2 Unchanged Medium
Q15417	P17ab5	calponin 3; acidic	911.495	603	737.1204	750.6841	-3.06E-01	-5.95E-01	2 Unchanged Medium
P52907	O08ab4	capicupa homolog (Drosophila)	629.0213	486	439.6052	518.1163	-5.17E-01	-3.73E-01	2 Unchanged Medium
Q9GZC3	N16gh1	carbohydrate (N-acetylglucosam	793.1054	684	584.7035	705.5063	-5.36E-01	-3.11E-01	2 Unchanged Medium
Q16619	K01ab4	cardiotrophin 1	1478.249	929	751.3352	824.5253	-7.81E-02	2.28E-01	2 Unchanged Medium
Q9UBD9	I24cd8	cardiotrophin-like cytokine; neut	361.4077	893	489.6592	581.3157	4.38E-01	1.30E+00	2 Unchanged Medium
Q15699	M16cd4	cartilage paired-class homeoprot	747.0317	596	1109.834	817.569	5.71E-01	-3.26E-01	2 Unchanged Medium
P48729	A22ab6	casein kinase 1; alpha 1	690.8551	1150	902.9474	914.9218	3.66E-01	7.36E-01	2 Unchanged Medium
P48730	L07ab4	casein kinase 1; delta	951.5238	1160	1111.571	1073.796	2.24E-01	2.84E-01	2 Unchanged Medium
P19138	L08ef5	casein kinase 2; alpha 1 polypep	483.6062	597	461.8036	513.9702	-6.66E-02	3.03E-01	2 Unchanged Medium
P49662	C12ef6	caspase 4; apoptosis-related cys	2013.957	2460	1017.425	1631.485	-9.85E-01	2.90E-01	2 Unchanged Medium
P21964	F19ef6	catechol-O-methyltransferase	657.5868	1170	1268.869	1046.831	8.63E-01	7.51E-01	2 Unchanged Medium
P26232	K01ef7	catenin (cadherin-associated pro	797.8639	717	810.257	774.9896	2.22E-02	-1.54E-01	2 Unchanged Medium
P35222	G07ef7	catenin (cadherin-associated pro	969.252	1290	1103.619	1121.277	1.87E-01	4.14E-01	2 Unchanged Medium
P07339	N23ef7	cathepsin D (lysosomal aspartyl)	1253.01	947	1133.879	1111.314	-1.44E-01	-4.04E-01	2 Unchanged Medium
Q99667	C18cd6	Cbp/p300-interacting transactiva	1293.915	1600	2245.133	1711.366	7.95E-01	3.02E-01	2 Unchanged Medium
P49715	N17ef6	CCAAT/enhancer binding protein	882.9323	884	1045.45	937.3612	2.44E-01	1.26E-03	2 Unchanged Medium
P53567	N22ab5	CCAAT/enhancer binding protein	826.9569	1160	1584.869	1191.643	9.38E-01	4.92E-01	2 Unchanged Medium
O95627	B21cd8	CCR4-NOT transcription complex	606.4629	851	692.4535	716.7046	1.91E-01	4.89E-01	2 Unchanged Medium
Q04900	G02cd4	CD164 antigen; slatmucin	750.3086	570	673.7234	664.5986	-1.55E-01	-3.97E-01	2 Unchanged Medium
P07766	P07ab3	CD3E antigen; epsilon polypeptid	1808.209	1410	2643.721	1953.844	5.48E-01	-3.59E-01	2 Unchanged Medium
P34810	A21ab4	CD68 antigen	2460.227	1100	1283.961	1617.586	-8.27E-01	-1.16E+00	2 Unchanged Medium
P18582	B21ab5	CD81 antigen (target of anti-prouf	1303.144	938	1598.276	1279.761	2.95E-01	-4.75E-01	2 Unchanged Medium
Q16181	F09ef5	CDC10 cell division cycle 10 hom	426.6642	443	751.3623	540.3444	8.16E-01	5.42E-02	2 Unchanged Medium
Q16543	H01ef5	CDC37 cell division cycle 37 hom	1085.897	1050	1336.155	1158.574	2.99E-01	-4.35E-02	2 Unchanged Medium
O14735	I14cd6	CDP-diacylglycerol-inositol 3-ph	241.7793	1180	311.7422	579.4931	3.67E-01	2.29E+00	2 Unchanged Medium
P30260	F13ef5	cell division cycle 27	1060.612	1470	1469.824	1334.733	4.70E-01	4.74E-01	2 Unchanged Medium
P49427	B12ef7	cell division cycle 34	762.5808	1300	766.6843	942.0784	7.74E-03	7.66E-01	2 Unchanged Medium
P29373	F01ef7	cellular retinoic acid binding prot	1226.236	803	1350.177	1126.373	1.39E-01	-6.11E-01	2 Unchanged Medium
P41208	F09ab5	centrin; EF-hand protein; 2	539.1633	572	676.8582	629.3345	3.28E-01	3.18E-01	2 Unchanged Medium
O00522	F05ab4	cerebral cavernous malformation	870.4309	631	723.1482	741.4654	-2.67E-01	-4.64E-01	2 Unchanged Medium

O15183	B12d3	CGG triplet repeat binding protel	402.949	610	883.3283	632.0808	1.13E+00	5.98E-01	2	Unchanged Medium
Q9Y225	D07ef2	CGI-06 protein	721.6709	674	1177.641	857.6492	7.06E-01	-9.94E-02	2	Unchanged Medium
Q9Y3C3	J05ef2	CGI-120 protein	1229.537	1360	2124.304	1572.302	7.89E-01	1.49E-01	2	Unchanged Medium
Q9Y3D0	J11ef2	CGI-128 protein	1592.767	2370	2011.685	1992.502	3.37E-01	5.75E-01	2	Unchanged Medium
Q9Y3E5	J17ef2	CGI-147 protein	532.425	788	567.0634	629.3057	9.09E-02	5.66E-01	2	Unchanged Medium
Q9Y3E8	C08ef2	CGI-150 protein	785.276	924	778.0449	829.1206	-1.33E-02	2.35E-01	2	Unchanged Medium
Q9Y320	A19ef2	CGI-31 protein	745.0314	932	703.7829	793.4541	-8.22E-02	3.22E-01	2	Unchanged Medium
Q9Y357	P16ef1	CGI-40 protein	817.7272	769	418.6337	668.441	-9.66E-01	-8.67E-02	2	Unchanged Medium
Q9Y360	A10ef2	CGI-45 protein	786.0567	914	796.6229	832.2061	1.83E-02	2.17E-01	2	Unchanged Medium
Q9Y512	B04ef3	CGI-51 protein	967.3508	859	1045.638	957.4201	1.12E-01	-1.71E-01	2	Unchanged Medium
Q9Y390	K21ef2	CGI-81 protein	1391.902	802	1140.01	1111.152	-2.68E-01	-7.96E-01	2	Unchanged Medium
P40227	N20ab4	chaperonin containing TCP1; sub	1011.613	436	592.4944	679.9043	-7.72E-01	-1.22E+00	2	Unchanged Medium
Q99832	H07cd6	chaperonin containing TCP1; sub	1190.644	1090	1548.874	1274.983	3.79E-01	-1.33E-01	2	Unchanged Medium
Q9UBR5	I23ef4	chemokine-like factor 1	1047.63	1800	1059.437	1303.798	1.62E-01	7.85E-01	2	Unchanged Medium
Q9UHN8	N05ef4	chemokine-like factor 1	1568.851	2030	1237.728	1611.343	-3.42E-01	3.70E-01	2	Unchanged Medium
P54105	L07ef5	chloride channel; nucleotide-ser	471.0775	487	640.6855	532.9217	4.44E-01	4.80E-02	2	Unchanged Medium
Q14781	F09ef1	chromobox homolog 2 (Pc class)	795.873	749	713.815	753.0305	-1.57E-01	-8.68E-02	2	Unchanged Medium
Q9BX54	K12cd5	chromosome 1 open reading fra	874.0189	1370	904.3066	1050.603	4.91E-02	6.52E-01	2	Unchanged Medium
Q9NP00	H07gh4	chromosome 11 hypothetical pro	998.8577	834	658.794	897.3389	-2.18E-01	-2.60E-01	2	Unchanged Medium
Q9UKR5	G14cd7	chromosome 14 open reading fra	1181.962	1160	1285.11	1207.747	1.21E-01	-3.18E-02	2	Unchanged Medium
P56378	M16cd5	chromosome 14 open reading fra	503.5233	690	690.9975	694.9486	8.23E-01	4.55E-01	2	Unchanged Medium
Q95433	B22cd7	chromosome 14 open reading fra	656.1775	563	439.8755	552.8428	-5.80E-01	-2.20E-01	2	Unchanged Medium
Q9NV31	J23gh3	chromosome 15 open reading fra	853.8367	832	861.2221	848.9729	1.24E-02	-3.76E-02	2	Unchanged Medium
Q9NVE2	D09gh3	chromosome 2 open reading fra	648.49	671	468.6352	598.0999	-4.69E-01	4.96E-02	2	Unchanged Medium
Q9U015	L04gh4	chromosome 20 open reading fra	2518.951	2140	1201.051	1952.881	-1.07E+01	-2.36E-01	2	Unchanged Medium
Q9P007	M09ef8	chromosome 20 open reading fra	581.9098	1080	1200.655	954.524	1.04E+00	8.93E-01	2	Unchanged Medium
Q9Y3B1	H22ef1	chromosome 20 open reading fra	1691.864	1230	783.7799	1235.108	-1.11E+00	-4.60E-01	2	Unchanged Medium
Q9BQ89	C01gh8	chromosome 20 open reading fra	1460.875	952	1221.732	1211.641	-2.58E-01	-8.17E-01	2	Unchanged Medium
Q96C58	J19gh7	chromosome 6 open reading fra	1254.647	1080	480.9999	940.0036	-1.38E+00	-2.10E-01	2	Unchanged Medium
Q9Y524	K12ef3	chromosome 6 open reading fra	915.3818	968	372.3119	758.6366	-1.30E+00	1.10E-01	2	Unchanged Medium
Q00610	H12cd5	clathrin; heavy polypeptide (Hc)	1639.759	1210	1437.44	1427.503	-1.90E-01	-4.44E-01	2	Unchanged Medium
P56749	F04cd7	claudin 12	2262.278	2480	1233.472	1992.755	-8.75E-01	1.34E-01	2	Unchanged Medium
Q43809	M15cd7	cleavage and polyadenylation sp	640.2301	503	683.3467	608.9825	9.40E-02	-3.47E-01	2	Unchanged Medium
O96005	G05ab4	clift lip and palate associated tra	1353.338	1170	1394.845	1304.597	4.36E-02	-2.15E-01	2	Unchanged Medium
Q16740	E20cd4	CipP caspase-like protease; ATP-	625.8711	528	475.0848	543.0367	-3.98E-01	-2.45E-01	2	Unchanged Medium
P55085	O24ab5	coagulation factor II (thrombin)	829.7537	979	392.7495	734	-1.08E+00	2.39E-01	2	Unchanged Medium
P13726	B05ab4	coagulation factor III (thrombopo	1079.841	880	442.6212	800.9723	-1.29E+00	-2.94E-01	2	Unchanged Medium
Q9Y678	D14ef8	coat protein gamma-cop	815.7993	738	1069.756	854.5161	3.08E-01	-1.45E-01	2	Unchanged Medium
Q15633	M11ef3	coated vesicle membrane prote	706.3054	804	870.2118	793.6589	3.01E-01	1.88E-01	2	Unchanged Medium
O43513	N06cd4	cocfactor required for Sp1 transcr	591.8619	481	798.8706	623.9284	4.33E-01	-2.99E-01	2	Unchanged Medium
Q9Y281	N18cd8	cofilin 2 (muscle)	671.9394	270	1093.534	678.6369	7.03E-01	-1.31E+00	2	Unchanged Medium
P04141	G22gh6	colony stimulating factor 2 (gran	116.2139	1290	165.718	522.783	5.12E-01	3.47E+00	2	Unchanged Medium
P02745	L06ef1	complement component 1; q sub	683.4431	1650	798.2366	1042.465	2.24E-01	1.27E+00	2	Unchanged Medium
P29279	I16ab4	connective tissue growth factor	596.4123	537	1071.517	734.8489	8.45E-01	-1.52E-01	2	Unchanged Medium
O43191	B02cd3	COP9 constitutive photomorph	855.8616	1030	1302.334	1062.925	6.06E-01	2.68E-01	2	Unchanged Medium
Q99627	C01cd7	COP9 homolog	788.2297	958	1195.497	984.0634	6.01E-01	2.97E-01	2	Unchanged Medium
O15387	G21cd7	COP9 subunit 6 (MOV34 homolo	590.9973	382	628.5041	533.8251	8.88E-02	-6.30E-01	2	Unchanged Medium
Q9ULV4	K18ef3	coronin; actin binding protein; 1C	1594.037	1200	1362.545	1385.839	-2.26E-01	-4.09E-01	2	Unchanged Medium
Q9BR76	I14gh7	coronin; actin-binding protein; 1E	708.5653	1080	690.8568	827.7884	-3.65E-02	6.13E-01	2	Unchanged Medium
Q14601	B22cd5	COX17 homolog; cytochrome c c	889.1581	1440	745.8658	1026.374	-2.54E-01	7.00E-01	2	Unchanged Medium
Q9Y682	E02ef8	CREBBP/EP300 inhibitory protel	946.9513	1030	1988.725	1323.308	1.07E+00	1.27E-01	2	Unchanged Medium
Q9NY68	C06gh4	CTL2 gene	1381.821	804	788.5002	991.4995	-8.09E-01	-7.81E-01	2	Unchanged Medium
P24385	O04ef5	cyclin D1 (PRAD1; parathyroid a	1214.611	2150	1100.478	1486.769	-1.42E-01	8.21E-01	2	Unchanged Medium
Q9NX4	K09gh2	cyclin M2	1560.659	1720	1582.768	1620.99	2.03E-02	1.40E-01	2	Unchanged Medium
P01034	I11ab6	cystatin C (amyloid angiopathy a	1067.127	970	1366.396	1134.612	3.57E-01	-1.37E-01	2	Unchanged Medium
Q15828	I13ab4	cystatin E/M	967.1669	2790	451.3932	1404.267	-1.10E+00	1.53E+00	2	Unchanged Medium
P01036	C02ab6	cystatin S	1261.605	466	1069.756	932.4892	-2.38E-01	-1.44E-00	2	Unchanged Medium
P52943	I05ab4	cysteine-rich protein 2	874.1939	499	1277.819	883.824	5.48E-01	-8.08E-01	2	Unchanged Medium
P13498	G18ab3	cytochrome b-245; alpha polype	708.9954	1050	359.3156	707.7483	-9.81E-01	5.73E-01	2	Unchanged Medium
P00167	C04ab6	cytochrome b-5	2187.128	1480	1034.311	1565.893	-1.08E+00	-5.67E-01	2	Unchanged Medium
P00001	N12gh6	cytochrome c	547.6708	442	517.6125	502.4766	-8.14E-02	-3.09E-01	2	Unchanged Medium
P10606	I24gh6	cytochrome c oxidase subunit Vb	1364.01	2100	2087.456	1851.225	6.14E-01	6.24E-01	2	Unchanged Medium
P08574	P10ab5	cytochrome c-1	667.9346	443	441.6771	517.4383	-5.97E-01	-5.93E-01	2	Unchanged Medium
Q99428	C17gh1	cytoskeleton-associated protein	550.9411	684	777.3269	673.9633	4.71E-01	2.85E-01	2	Unchanged Medium
Q07065	G13cd7	cytoskeleton-associated protein	602.5101	575	1785.415	987.5887	1.57E+00	-6.78E-02	2	Unchanged Medium
Q15038	L13ef3	DAZ associated protein 2	808.0755	890	564.7611	754.4305	-5.17E-01	1.40E-01	2	Unchanged Medium
Q9H2L4	B18gh8	DC32	408.0427	702	780.2878	630.0414	9.35E-01	7.82E-01	2	Unchanged Medium
Q9NPAB	G22gh7	DC6 protein	944.3094	1570	1514.164	1342.189	6.81E-01	7.32E-01	2	Unchanged Medium
Q60231	H13cd3	DEAD/H (Asp-Glu-Ala-Asp/His) t	753.8815	873	799.6561	808.7915	8.50E-02	2.11E-01	2	Unchanged Medium
Q9GZR7	E02gh4	DEAD/H (Asp-Glu-Ala-Asp/His) t	803.42	984	774.3765	854.0955	-5.31E-02	2.93E-01	2	Unchanged Medium
P17844	F04ab4	DEAD/H (Asp-Glu-Ala-Asp/His) t	1482.642	1440	1670.104	1503.749	1.72E-01	-4.26E-02	2	Unchanged Medium
Q08211	M03ab4	DEAD/H (Asp-Glu-Ala-Asp/His) t	907.5859	658	907.4343	824.2193	-2.41E-04	-4.65E-01	2	Unchanged Medium
Q9UVJ9	D08ef2	DEAD-box protein abstract	976.8378	1230	870.3672	1024.437	-1.66E-01	3.28E-01	2	Unchanged Medium
P51398	G18ef6	death associated protein 3	920.3044	981	814.3518	905.1904	-1.76E-01	9.20E-02	2	Unchanged Medium
Q13437	G22cd4	Deleted in split-hand/split-foot 1	1565.344	1500	1721.672	1596.672	1.37E-01	-5.88E-02	2	Unchanged Medium
O60735	O05cd6	dendritic cell protein	858.6375	502	467.3433	609.2393	-8.78E-01	-7.75E-01	2	Unchanged Medium
Q16854	M05ab5	deoxyguanosine kinase	858.1918	885	989.3036	910.8082	2.05E-01	4.43E-02	2	Unchanged Medium
Q9Y295	H04ab8	developmentally regulated GTP I	736.3786	634	660.7023	676.9267	-1.56E-01	-2.17E-01	2	Unchanged Medium
P00387	F09ab3	diaphorase (NADH) (cytochrome	1402.134	1030	1435.74	1290.593	3.42E-02	-4.40E-01	2	Unchanged Medium
Q9UHV9	I08ef2	dicarbonyl L-xylulose reductase	544.2125	740	838.7807	741.1	7.87E-01	4.44E-01	2	Unchanged Medium
P36557	C06ab6	dihydrofolic acid S-succinyltrans	625.9037	713	393.7165	577.6196	-6.69E-01	1.88E-01	2	Unchanged Medium
Q99075	M12ef7	diphtheria toxin receptor (heparf	721.8431	638	197.117	518.9525	-1.87E-00	-1.78E-01	2	Unchanged Medium
Q9UFNH	H10gh6	DKFZP564B147 protein	966.5927	947	1469.105	1127.658	6.04E-01	-2.91E-02	2	Unchanged Medium
Q95882	C13ef8	DKFZP564C1940 protein	941.4076	865	804.639	870.3185	-2.26E-01	-1.22E-01	2	Unchanged Medium
Q9Y269	C07ef8	DKFZP564M082 protein	675.8991	1110	1208.543	998.4411	8.38E-01	7.17E-01	2	Unchanged Medium
Q9NW3	J11ef8	DKFZP566C243 protein	419.5607	770	625.8483	605.084	5.77E-01	8.76E-01	2	Unchanged Medium

Q9H6Y7	H04gh6	DKFZP566H073 protein	1390.389	1480	1191.195	1352.292	-2.23E-01	8.55E-02	2 Unchanged Medium
Q9Y3X0	P23ef8	DKFZP566M1019 protein	588.3603	505	672.4872	588.5767	1.93E-01	-2.21E-01	2 Unchanged Medium
O50762	G19cd4	dolichyl-phosphate mannosyliran	407.0059	581	605.8353	531.3373	5.74E-01	5.14E-01	2 Unchanged Medium
P53805	B11ab5	Down syndrome critical region gr	370.0907	663	511.9248	515.0794	4.68E-01	8.42E-01	2 Unchanged Medium
Q13597	N13e3	downregulated in ovarian cancer	594.6931	693	623.702	636.966	6.87E-02	2.20E-01	2 Unchanged Medium
Q9C005	J05gh8	dpy-30-like protein	610.4585	1210	1174.001	1064.132	5.35E-01	5.76E-01	2 Unchanged Medium
Q13448	J03cd6	DR1-associated protein 1 (negat)	1240.359	1140	2382.895	1586.247	9.42E-01	-1.27E-01	2 Unchanged Medium
Q9UHF9	K01ef4	dual oxidase 2	1146.14	648	316.6462	703.5318	-1.86E+00	-8.23E-01	2 Unchanged Medium
P51452	N22ab4	dual specificity phosphatase 3 (v	649.6813	605	473.5652	576.1845	-4.56E-01	-1.02E-01	2 Unchanged Medium
Q14203	A13ab6	dynactin 1 (p150; glued homolog	507.5942	529	623.6948	553.5576	2.97E-01	6.06E-02	2 Unchanged Medium
Q13561	D19qd6	dynactin 2 (p50)	1565.587	1380	1173.024	1372.261	-4.16E-01	-1.84E-01	2 Unchanged Medium
Q13409	I16ef1	dynamin; cytoplasmic; intermediate	793.3207	604	464.9757	620.6506	-7.71E-01	-3.94E-01	2 Unchanged Medium
Q09472	C18ab4	E1A binding protein p300	1496.409	2120	1342.944	1651.644	-1.56E-01	5.00E-01	2 Unchanged Medium
	D20gh8	EA1 protein	642.1587	652	469.6834	588.0816	-4.51E-01	2.28E-02	2 Unchanged Medium
P78365	N19ab4	early development regulator 2 (p	894.3715	1070	761.5923	907.5945	-2.32E-01	2.54E-01	2 Unchanged Medium
Q99848	G11od7	EBNA1 binding protein 2	977.8871	611	818.6583	802.3778	-2.56E-01	-6.79E-01	2 Unchanged Medium
Q12805	A21ab6	EGF-containing fibulin-like extra	1002.62	332	458.9563	597.7763	-1.13E+00	-1.60E+00	2 Unchanged Medium
Q9Y613	D21od8	EH domain-binding mitotic phosph	738.8984	500	629.1845	621.9752	-2.28E-01	-5.60E-01	2 Unchanged Medium
Q15717	C04ab4	ELAV (embryonic lethal; abnorm	850.8493	800	843.4463	831.3485	-1.26E-02	-8.94E-02	2 Unchanged Medium
P13804	I24ab3	electron-transfer-flavoprotein; alp	918.8391	545	529.2866	664.3533	-7.96E-01	-7.54E-01	2 Unchanged Medium
Q14247	K17ef6	ems 1 sequence (mammary tumor	1135.188	1050	1002.084	1063.9	-1.80E-01	-1.06E-01	2 Unchanged Medium
P42892	O21ab4	endothelin converting enzyme 1	602.4294	799	809.7071	737.1982	4.27E-01	4.08E-01	2 Unchanged Medium
P30084	A17ab6	enoyl Coenzyme A hydratase; sh	802.3114	1210	741.2226	917.9548	-1.14E-01	5.93E-01	2 Unchanged Medium
P07099	I20ab3	epoxide hydrolase 1; microsomal	1231.48	1840	1198.169	1424.661	-3.96E-02	5.83E-01	2 Unchanged Medium
P29692	H04ab5	eukaryotic translation elongation	1329.756	744	1110.87	1061.631	-2.59E-01	-8.37E-01	2 Unchanged Medium
P20042	L05cd4	eukaryotic translation initiation fa	1489.433	603	956.276	1016.24	-6.39E-01	-1.30E+00	2 Unchanged Medium
P41091	A20ab4	eukaryotic translation initiation fa	742.5843	474	478.7249	565.2535	-6.33E-01	-6.46E-01	2 Unchanged Medium
Q99613	K16cd3	eukaryotic translation initiation fa	1140.022	853	998.7488	997.2011	-1.91E-01	-4.19E-01	2 Unchanged Medium
P78344	C02ab4	eukaryotic translation initiation fa	1562.952	1520	1177.845	1419.665	-4.08E-01	-4.19E-02	2 Unchanged Medium
P23588	A24ab4	eukaryotic translation initiation fa	1343.019	1010	1125.825	1160.659	-2.54E-01	-4.07E-01	2 Unchanged Medium
Q13541	C03ab5	eukaryotic translation initiation fa	1655.926	1060	2293.236	1669.873	4.70E-01	-6.43E-01	2 Unchanged Medium
Q13542	A19ab6	eukaryotic translation initiation fa	1620.111	1850	1663.197	1712.605	3.79E-02	1.95E-01	2 Unchanged Medium
O60573	G16cd5	eukaryotic translation initiation fa	799.7789	883	819.3679	833.9147	3.49E-02	1.42E-01	2 Unchanged Medium
Q16394	K02ab3	exostoses (multiple) 1	513.7526	428	813.2693	584.9471	6.63E-01	-2.64E-01	2 Unchanged Medium
P37268	C17ab6	farnesyldiphosphate farnesyltr	726.0862	455	649.0518	610.2033	-1.62E-01	-6.73E-01	2 Unchanged Medium
P55899	L22ab5	Fc fragment of IgG; receptor; trai	450.8629	771	476.1039	566.0193	7.86E-02	7.74E-01	2 Unchanged Medium
Q9UK73	P05ef3	Fem-1 homolog b (C. elegans)	548.2677	547	530.801	541.9489	-4.67E-02	-3.93E-03	2 Unchanged Medium
P21333	G14ab4	filamin A; alpha (actin binding pro	946.0465	675	1277.458	966.2982	4.33E-01	-4.86E-01	2 Unchanged Medium
P26885	P07ab4	FK506 binding protein 2 (13kD)	814.6357	510	661.4593	662.0387	-3.01E-01	-6.76E-01	2 Unchanged Medium
Q13451	F15ab4	FK506 binding protein 5	1366.805	1110	812.8568	1097.248	-7.50E-01	-2.98E-01	2 Unchanged Medium
O95633	M01cd6	folistatin-like 3 (secreted glycop	1312.174	1280	1092.99	1227.557	-2.64E-01	-3.86E-02	2 Unchanged Medium
P15407	A20cd4	FOS-like antigen 1	1696.135	1350	1218.491	1421.01	-4.77E-01	-3.31E-01	2 Unchanged Medium
Q14192	G02ab4	four and a half LIM domains 2	309.9219	591	1210.635	703.7424	1.97E+00	9.30E-01	2 Unchanged Medium
Q9NZ40	N17gh6	fuse-binding protein-Interacting r	924.2347	911	1110.468	981.791	2.65E-01	-2.13E-02	2 Unchanged Medium
P35637	P19ab4	fusion; derived from l(1';2';16) rna	866.3996	654	1159.792	893.3381	4.21E-01	-4.06E-01	2 Unchanged Medium
	E21gh7	FXYD domain-containing ion trar	942.6126	1060	802.8679	935.6666	-2.32E-01	1.71E-01	2 Unchanged Medium
Q9Y653	B02cd5	G protein-coupled receptor 56	2010.489	2160	1501.617	1889.081	-4.21E-01	1.00E-01	2 Unchanged Medium
Q9H1C0	E18gh4	G protein-coupled receptor 92	712.1007	750	719.7999	727.2869	1.55E-02	7.47E-02	2 Unchanged Medium
P15170	L13ab4	G1 to S phase transition 1	2042.425	1410	1109.721	1521.226	-8.80E-01	-5.33E-01	2 Unchanged Medium
O95165	D09cd7	GABA(A) receptor-associated pro	1260.495	2210	1227.378	1572.36	-6.11E-01	7.87E-01	2 Unchanged Medium
O08765	D21cd7	GABA(A) receptor-associated pro	1241.27	1130	918.8337	1095.839	-4.34E-01	-1.39E-01	2 Unchanged Medium
P16278	O05ef1	galactosidase; beta 1	539.4222	600	656.0518	665.3025	2.82E-01	5.69E-01	2 Unchanged Medium
P78537	J23ab4	GCN5 general control of amino-	813.3309	637	919.5196	790.0409	1.77E-01	-3.52E-01	2 Unchanged Medium
P31150	F14ab4	GDP dissociation inhibitor 1	633.6157	894	640.108	722.7008	1.07E-02	4.97E-01	2 Unchanged Medium
P06396	B23ab3	gelsolin (amyloidosis; Finnish typ	330.1567	577	633.2269	513.4286	9.40E-01	8.05E-01	2 Unchanged Medium
P52657	E03ab6	general transcription factor II A; 2	538.6557	685	700.1857	641.1721	3.78E-01	3.46E-01	2 Unchanged Medium
Q00403	F08ef6	general transcription factor II B	500.4565	791	454.8328	582.2035	-1.38E-01	6.61E-01	2 Unchanged Medium
P48060	I23cd7	glioma pathogenesis-related prot	676.4844	692	752.7928	707.2232	1.54E-01	3.35E-02	2 Unchanged Medium
P05744	B19ab3	glucose phosphate isomerase	900.9772	553	726.4749	726.7688	-3.11E-01	-7.05E-01	2 Unchanged Medium
P30101	G13ab5	glucose regulated protein; 58kD	1708.658	1250	2220.105	1726.668	3.78E-01	-4.50E-01	2 Unchanged Medium
O43363	I22ef1	glutamate receptor; ionotropic; N	1729.777	1890	1655.131	1758.853	-6.36E-02	1.29E-01	2 Unchanged Medium
P15104	H22ab5	glutamate-ammonia ligase (gluta	1170.59	1040	1180.088	1130.151	1.17E-02	-1.71E-01	2 Unchanged Medium
Q06210	A23ab5	glutamine-fructose-6-phosphate I	869.494	600	863.157	777.6585	-1.06E-02	-5.34E-01	2 Unchanged Medium
Q9Y3D4	M19ef2	glutaredoxin 2	888.5406	894	1099.209	960.4756	3.07E-01	8.32E-03	2 Unchanged Medium
Q9Y203	C24ef2	glutathione S-transferase subunit	841.3959	346	414.7892	533.8957	-1.02E+00	-1.28E+00	2 Unchanged Medium
P48637	D01ab3	glutathione synthetase	650.8496	429	488.6663	522.9685	-4.13E-01	-6.00E-01	2 Unchanged Medium
P78417	E20cd5	glutathione-S-transferase like; glt	1983.626	2020	1805.489	1937.888	-1.36E-01	2.95E-02	2 Unchanged Medium
P49840	J14ef4	glycogen synthase kinase 3 alpha	1057.368	1460	1247.816	1254.087	2.39E-01	4.63E-01	2 Unchanged Medium
P13224	F23ab3	glycoprotein Ib (platelet); beta pc	487.4684	530	653.4727	557.0977	4.23E-01	1.22E-01	2 Unchanged Medium
Q9UBQ7	L08cd7	glyoxylate reductase/hydroxypyru	947.0262	977	997.593	973.9926	7.50E-02	4.55E-02	2 Unchanged Medium
Q9P271	C02ef2	GMPR2 for guanosine monopho	762.0126	1070	817.0496	882.4154	1.01E-01	4.87E-01	2 Unchanged Medium
Q9H446	I04gh5	golgi phosphoprotein 3 (coal-pro	1027.603	1210	1209.783	1148.94	2.35E-01	2.35E-01	2 Unchanged Medium
P28799	B19ab5	granulin	1611.298	1750	1238.745	1532.188	-3.79E-01	1.16E-01	2 Unchanged Medium
Q14393	H10ab3	growth arrest-specific 6	484.4849	563	739.1661	595.5619	6.09E-01	2.17E-01	2 Unchanged Medium
P29354	H06ef5	growth factor receptor-bound pro	721.5894	654	663.0587	746.3732	-1.22E-01	2.44E-01	2 Unchanged Medium
Q14451	D20ab4	growth factor receptor-bound pro	712.3296	846	636.8962	731.6029	-1.61E-01	2.47E-01	2 Unchanged Medium
Q9Y6G2	E04ef8	growth hormone inducible transr	1289.256	1020	974.263	1093.42	-4.04E-01	-3.43E-01	2 Unchanged Medium
P04899	J09ab4	guanine nucleotide binding prote	860.9208	1390	1748.649	1334.01	1.02E+00	6.94E-01	2 Unchanged Medium
P11016	M13ef5	guanine nucleotide binding prote	758.629	773	836.6295	789.4586	1.41E-01	2.73E-02	2 Unchanged Medium
P13905	G09ab6	guanine nucleotide-releasing fac	410.0949	569	535.1869	504.61	3.84E-01	4.71E-01	2 Unchanged Medium
Q16774	L16ab3	guanylate kinase 1	968.5867	1340	975.8911	1095.967	1.08E-02	4.72E-01	2 Unchanged Medium
Q9Y649	K16ef4	GW128 protein	1663.305	2420	1834.174	1971.464	1.41E-01	5.39E-01	2 Unchanged Medium
P07305	G13ab6	H1 histone family; member 0	1780.353	1870	1746.555	1797.448	-2.77E-02	6.73E-02	2 Unchanged Medium
O75367	M14cd5	H2A histone family; member Y	1065.311	837	455.5967	786.0181	-1.23E+00	-3.48E-01	2 Unchanged Medium
P17317	C24ab6	H2A histone family; member Z	591.0013	461	1570.489	874.2269	1.41E+00	-3.58E-01	2 Unchanged Medium
P02278	M16gh6	H2B histone family; member G	586.8773	852	684.8287	707.973	2.22E-01	5.38E-01	2 Unchanged Medium

Q9NS37	A03gh5	HCF-binding transcription factor	857.3143	717	601.7268	725.1835	-5.11E-01	-2.59E-01	2	Unchanged	Medium
O96004	E02cd5	heart and neural crest derivative	705.5163	612	621.033	646.3401	-1.84E-01	-2.04E-01	2	Unchanged	Medium
P10809	M11ef5	heat shock 60kD protein 1 (chaperone)	1693.23	1020	1276.41	1330.235	-4.08E-01	-7.30E-01	2	Unchanged	Medium
P34932	I11ef1	heat shock 70kD protein 4	1402.505	1610	1042.113	1352.283	-4.28E-01	2.01E-01	2	Unchanged	Medium
P07900	G16ef7	heat shock 90kD protein 1; alpha	2405.793	1430	1512.258	1783.374	-6.70E-01	-7.48E-01	2	Unchanged	Medium
P08238	B20ab7	heat shock 90kD protein 1; beta	2781.462	1950	979.1145	1903.993	-1.51E+00	-5.11E-01	2	Unchanged	Medium
O75506	H17ab6	heat shock factor binding protein	1132.126	1300	1081.748	1171.256	-6.57E-01	1.99E-01	2	Unchanged	Medium
Q9UHG4	K18ef4	heme-regulated initiation factor 2	413.2841	659	576.3971	549.5035	4.80E-01	6.73E-01	2	Unchanged	Medium
P09105	J21ab4	hemoglobin; theta 1	702.445	484	769.2336	651.9692	-1.31E-01	-5.37E-01	2	Unchanged	Medium
O43504	D23cd5	hepatitis B virus x interacting protein	1008.655	1340	949.0116	1097.672	-8.79E-02	4.05E-01	2	Unchanged	Medium
Q9H216	N10gh5	hepatitis C virus core-binding protein	676.7297	620	473.9328	590.1783	-5.14E-01	-1.27E-01	2	Unchanged	Medium
P51858	K16ef7	hepatoma-derived growth factor I	894.1008	1170	490.7456	850.7213	-8.65E-01	3.85E-01	2	Unchanged	Medium
Q04150	A08ab7	heterogeneous nuclear ribonucleic acid	943.3857	870	1065.597	959.787	1.76E-01	-1.16E-01	2	Unchanged	Medium
Q13151	E15cd7	heterogeneous nuclear ribonucleic acid	906.986	944	1143.552	998.1703	3.34E-01	5.77E-02	2	Unchanged	Medium
P22626	N09ab6	heterogeneous nuclear ribonucleic acid	1021.87	1010	1584.855	1206.298	6.33E-01	-1.38E-02	2	Unchanged	Medium
P07910	A10ab7	heterogeneous nuclear ribonucleic acid	747.5309	718	1059.349	841.6601	5.03E-01	-5.79E-02	2	Unchanged	Medium
O14979	L09cd5	heterogeneous nuclear ribonucleic acid	1057.699	1990	1646.172	1563.717	6.38E-01	9.10E-01	2	Unchanged	Medium
P52597	G06ab7	heterogeneous nuclear ribonucleic acid	1902.939	1280	1517.274	1567.536	-3.27E-01	-5.69E-01	2	Unchanged	Medium
Q07244	N13ab6	heterogeneous nuclear ribonucleic acid	847.6967	667	684.4978	733.1055	-3.09E-01	-3.46E-01	2	Unchanged	Medium
Q15584	P03ab7	heterogeneous nuclear ribonucleic acid	725.3651	569	858.2829	717.4409	2.43E-01	-3.51E-01	2	Unchanged	Medium
P12081	J12ab4	histidyl-tRNA synthetase	555.5578	565	424.3904	514.8575	-3.89E-01	2.34E-02	2	Unchanged	Medium
Q9UBN7	E11cd8	histone deacetylase 6	685.5336	407	695.1552	595.8457	2.01E-02	-7.53E-01	2	Unchanged	Medium
Q13038	M07cd4	HLA-B associated transcript 1	681.4666	604	921.7532	735.5784	4.36E-01	-1.75E-01	2	Unchanged	Medium
Q99873	H02ef7	HMT1 hnRNP methyltransferase	690.1184	836	1209.872	978.6584	4.43E-01	-9.05E-02	2	Unchanged	Medium
Q9H053	M14gh8	homolog of yeast MAF1	744.9951	921	1013.86	893.139	4.45E-01	3.05E-01	2	Unchanged	Medium
P51610	L21ab5	host cell factor C1 (VP16-access)	583.7478	580	735.1691	632.9765	3.33E-01	-9.25E-03	2	Unchanged	Medium
O00165	I04cd6	HS1 binding protein	1482.068	1490	2425.818	1800.489	7.11E-01	1.12E-02	2	Unchanged	Medium
Q9Y205	P24ef7	HSPC003 protein	620.7783	1010	625.6574	752.165	1.13E-02	7.02E-01	2	Unchanged	Medium
Q9Y2R0	A05ef8	HSPC009 protein	1507.005	1720	1784.562	1668.909	2.44E-01	1.87E-01	2	Unchanged	Medium
Q9Y2T0	A17ef8	HSPC022 protein	453.0964	733	326.4215	504.1821	-4.73E-01	6.94E-01	2	Unchanged	Medium
Q9UNZ5	C17ef8	HSPC023 protein	825.3888	1310	1347.488	1159.538	7.07E-01	6.62E-01	2	Unchanged	Medium
Q9P032	O19ef8	HSPC125 protein	558.6905	602	843.0953	668.1435	5.93E-01	1.08E-01	2	Unchanged	Medium
Q9P019	A05ef6	HSPC141 protein	717.9096	1700	1519.292	1312.254	1.08E+00	1.24E+00	2	Unchanged	Medium
Q9P004	A24ef8	HSPC160 protein	1182.006	1070	545.8523	932.7666	-1.11E+00	-1.43E-01	2	Unchanged	Medium
Q9P003	C04ef8	HSPC163 protein	801.5204	1410	1148.378	1118.827	5.19E-01	8.11E-01	2	Unchanged	Medium
Q9P000	C06ef8	HSPC166 protein	508.2074	921	523.3806	650.7428	4.24E-02	8.57E-01	2	Unchanged	Medium
Q9Y684	N09ef2	HSPC034 protein	569.9533	628	797.4619	665.044	4.85E-01	1.39E-01	2	Unchanged	Medium
Q9NRG2	D01gh4	HTGN29 protein	1276.132	1470	1639.451	1462.8	3.61E-01	2.07E-01	2	Unchanged	Medium
Q16775	G15ab6	hydroxycetyl glutathione hydrolase	511.3412	676	407.0538	531.4885	-3.29E-01	4.03E-01	2	Unchanged	Medium
P40939	D07ab3	hydroxycetyl-Coenzyme A hydratase	1814.498	1770	1617.578	1733.575	-1.66E-01	-3.69E-02	2	Unchanged	Medium
P55064	D09ab3	hydroxycetyl-Coenzyme A hydratase	539.2691	890	1218.105	682.3271	1.18E+00	7.22E-01	2	Unchanged	Medium
Q14526	B13ab5	hypermethylated in cancer 1	918.3678	904	1008.759	943.6552	1.35E-01	-2.30E-02	2	Unchanged	Medium
Q9UBS2	A15ef5	hyperpodanization activated cyclin	676.9289	688	520.6835	628.6277	-3.79E-01	2.40E-02	2	Unchanged	Medium
Q9EWB8	P08gh8	hypothetical gene ZDS2F10	727.4433	605	223.8014	518.5988	-1.70E+00	-2.67E-01	2	Unchanged	Medium
Q9Y256	D01ef2	hypothetical protein	1188.199	1490	1593.015	1423.598	4.23E-01	3.26E-01	2	Unchanged	Medium
Q9UKZ1	I23gh3	hypothetical protein C40	657.2427	614	506.0272	592.3978	-3.77E-01	-9.84E-02	2	Unchanged	Medium
Q9UJJ9	D21gh8	hypothetical protein CAB56184	432.491	695	601.25	576.3525	4.75E-01	6.85E-01	2	Unchanged	Medium
Q95891	D08ef2	hypothetical protein CL25022	1675.198	2070	1477.523	1741.841	-1.81E-01	3.07E-01	2	Unchanged	Medium
Q9UJJ9	F08gh6	hypothetical protein DJ328E19.C	1119.481	935	1005.691	1019.924	-1.55E-01	-2.60E-01	2	Unchanged	Medium
Q9H0L3	K20gh8	hypothetical protein DKFZp564K	1287.049	1080	1149.302	1169.228	-1.68E-01	-2.59E-01	2	Unchanged	Medium
Q9NWDB	N05gh2	hypothetical protein FLJ10099	754.9838	758	710.8818	741.1753	-6.68E-02	5.11E-03	2	Unchanged	Medium
Q9NW90	P21gh2	hypothetical protein FLJ10211	492.5962	551	601.7235	548.3816	2.89E-01	1.61E-01	2	Unchanged	Medium
Q9NW61	B18gh2	hypothetical protein FLJ10297	772.0358	844	620.6513	745.7235	-3.14E-01	1.29E-01	2	Unchanged	Medium
Q9NW16	G04gh3	hypothetical protein FLJ10374	756.2846	543	467.9722	589.0741	-6.93E-01	-4.78E-01	2	Unchanged	Medium
Q9NVZ3	G14gh3	hypothetical protein FLJ10420	437.615	702	362.923	500.7932	-2.70E-01	6.81E-01	2	Unchanged	Medium
Q9NVC3	D23gh3	hypothetical protein FLJ10815	1402.842	928	598.595	976.6359	-1.23E+00	-5.95E-01	2	Unchanged	Medium
Q9H9K7	B10gh5	hypothetical protein FLJ12681	446.1454	657	593.5606	565.6072	4.12E-01	5.59E-01	2	Unchanged	Medium
Q9H8H4	H06gh5	hypothetical protein FLJ12800	1058.023	775	1421.894	1084.852	4.26E-01	-4.50E-01	2	Unchanged	Medium
Q9P0R5	L02ef1	hypothetical protein FLJ14868	702.1841	684	1117.168	834.4521	6.70E-01	-3.78E-02	2	Unchanged	Medium
Q9NXQ4	M07gh3	hypothetical protein FLJ20113	1503.987	1520	1545.141	1521.653	3.89E-02	1.13E-02	2	Unchanged	Medium
Q9NXI2	M21gh3	hypothetical protein FLJ20234	643.4985	877	170.0291	566.3149	-1.85E+00	4.47E-01	2	Unchanged	Medium
Q9NXD5	E18gh2	hypothetical protein FLJ20309	617.1482	1420	758.0334	932.5386	2.97E-01	1.20E+00	2	Unchanged	Medium
Q9NX64	I18gh2	hypothetical protein FLJ20419	938.8958	825	981.8359	915.2399	6.42E-02	-1.86E-01	2	Unchanged	Medium
Q9NWV1	A20gh3	hypothetical protein FLJ20552	1366.306	1800	1533.352	1565.249	1.66E-01	3.95E-01	2	Unchanged	Medium
Q9NW78	D11gh2	hypothetical protein FLJ20608	980.6383	915	907.2393	934.2965	-1.12E-01	-9.99E-02	2	Unchanged	Medium
Q9NWM3	C20gh3	hypothetical protein FLJ20739	381.202	593	689.893	554.671	8.56E-01	6.37E-01	2	Unchanged	Medium
Q9H7C7	D05gh5	hypothetical protein FLJ21044	551.5395	708	585.1487	615.0164	8.53E-02	3.81E-01	2	Unchanged	Medium
Q9H6R6	J23gh5	hypothetical protein FLJ21952	425.3152	396	679.1125	500.0538	6.75E-01	-1.04E-01	2	Unchanged	Medium
Q9H873	F11gh5	hypothetical protein FLJ22548	1394.825	1220	530.5646	1047.134	-1.39E-01	-1.98E-01	2	Unchanged	Medium
Q95476	H15ef8	hypothetical protein HSA01916	1310.097	1040	1485.684	1279.962	1.81E-01	-3.27E-01	2	Unchanged	Medium
Q9Y244	B23ef2	hypothetical protein HSPC014	1668.101	1530	1243.802	1481.658	-4.23E-01	-1.22E-01	2	Unchanged	Medium
Q9P022	P04ef2	hypothetical protein HSPC138	666.1765	521	643.5979	610.0993	-4.97E-02	-3.56E-01	2	Unchanged	Medium
Q9P013	P06ef2	hypothetical protein HSPC148	916.5214	1450	1133.279	1157.03	3.06E-01	6.63E-01	2	Unchanged	Medium
Q9P009	P14ef2	hypothetical protein HSPC155	1031.658	1330	662.2481	1008.218	-6.40E-01	3.67E-01	2	Unchanged	Medium
Q9P0S9	A19ef3	hypothetical protein HSPC194	1336.172	1570	1957.055	1622.151	5.51E-01	2.36E-01	2	Unchanged	Medium
Q9NP10	A23ef3	hypothetical protein HSPC195	280.0356	644	672.088	532.0086	1.26E+00	1.20E+00	2	Unchanged	Medium
Q95887	C18ef2	hypothetical protein LOC51081	777.5591	709	551.8354	679.3595	-4.95E-01	-1.34E-01	2	Unchanged	Medium
Q9POT9	K02ef2	hypothetical protein LOC51234	1224.056	1290	1457.544	1322.295	2.52E-01	7.04E-02	2	Unchanged	Medium
Q9P0Q1	K10ef2	hypothetical protein LOC51248	376.8259	933	1014.441	774.623	1.43E+00	1.31E+00	2	Unchanged	Medium
Q9P0P0	K20ef2	hypothetical protein LOC51255	1301.286	2190	1904.375	1798.292	5.49E-01	7.50E-01	2	Unchanged	Medium
Q9P0N9	K22ef2	hypothetical protein LOC51256	540.326	374	604.1319	506.0883	1.61E-01	-5.32E-01	2	Unchanged	Medium
Q9NZD9	M23ef2	hypothetical protein LOC51323	600.1582	715	506.8479	607.2015	-2.44E-01	2.52E-01	2	Unchanged	Medium
O75207	M02gh4	hypothetical protein LOC57019	663.8685	644	680.7704	663.0017	3.83E-02	-4.30E-02	2	Unchanged	Medium
Q9BWLO	L24gh7	hypothetical protein MGC5244	569.8856	436	732.9891	579.5932	3.63E-01	-3.87E-01	2	Unchanged	Medium
Q9BW61	C09gh6	hypothetical protein MGC2594	1446.395</td								

Q9BQD3	E17gh6	hypothetical protein MGC2749	841.5499	889	899.9017	876.8925	9.67E-02	7.95E-02	2	Unchanged Medium
Q9BQ61	A05gh6	hypothetical protein MGC2803	1234.395	2170	1980.421	1784.728	6.62E-01	8.13E-01	2	Unchanged Medium
Q9BTY4	O23gh6	hypothetical protein MGC3222	561.6572	502	563.5781	548.9637	5.52E-02	-1.63E-01	2	Unchanged Medium
Q9BVX2	C17gh6	hypothetical protein MGC5576	747.2749	762	604.3725	704.7107	-3.06E-01	2.91E-02	2	Unchanged Medium
Q9H773	H17gh6	hypothetical protein MGC5627	799.182	819	584.0079	734.1306	-4.53E-01	3.57E-02	2	Unchanged Medium
Q9BPX5	L02gh7	hypothetical protein similar to ad	583.4076	424	632.4101	546.6359	1.16E-01	-4.60E-01	2	Unchanged Medium
Q9UJX8	B09ef3	hypothetical protein; estradiol-int	1184.334	948	1116.899	1083.179	-8.46E-02	-3.21E-01	2	Unchanged Medium
P00492	P12cd6	hypoxanthine phosphoribosyltransferase	1210.895	233	566.0945	669.9437	-1.10E+00	-2.38E+00	2	Unchanged Medium
P22304	I04ab6	iduronate 2-sulfatase (Hunter syn)	1197.3	1320	1095.895	1205.085	-1.28E-01	1.43E-01	2	Unchanged Medium
Q03827	F02ef6	immediate early protein	650.6358	537	536.2705	574.4895	-2.79E-01	-2.78E-01	2	Unchanged Medium
P12268	F11ab6	IMP (inosine monophosphate) de	1254.916	567	1293.693	1038.44	4.39E-02	-1.15E+00	2	Unchanged Medium
Q9Y6K9	P03cd3	Inhibitor of kappa light polypeptid	822.3859	788	807.6888	805.9933	-2.60E-02	-6.18E-02	2	Unchanged Medium
Q14573	F04eb6	inositol 1,4,5-triphosphate receptor	555.8397	646	627.6143	609.9521	1.75E-01	2.17E-01	2	Unchanged Medium
O15537	L09ab6	inositol polyphosphate phosphatase	997.7512	1150	1290.473	1146.822	3.71E-01	2.08E-01	2	Unchanged Medium
O15503	B05ab7	insulin induced gene 1	472.0202	428	615.7553	505.2037	3.84E-01	-1.42E-01	2	Unchanged Medium
PS2945	L13gh6	insulin upstream factor 1	1437.285	3700	746.514	1961.135	-9.45E-01	1.36E+00	2	Unchanged Medium
P51460	B07eb7	insulin-like 3 (Leydig cell)	1227.459	1290	1040.851	1184.891	-2.38E-01	6.76E-02	2	Unchanged Medium
P46977	D20ab6	integral membrane protein 1	1693.474	1790	2514.977	1998.711	5.71E-01	7.81E-02	2	Unchanged Medium
Q13418	H08ef5	integrin-linked kinase	1340.442	962	1599.336	1300.502	2.55E-01	-4.79E-01	2	Unchanged Medium
P48551	O21e7	interferon (alpha; beta and omega	605.1613	669	389.178	554.33	-6.37E-01	1.44E-01	2	Unchanged Medium
P15260	A02ef7	interferon gamma receptor 1	1165.784	2600	1179.083	1648.504	1.64E-02	1.16E+00	2	Unchanged Medium
P38484	D12ef5	interferon gamma receptor 2 (Int	593.8133	773	550.2576	638.9669	-1.10E-01	3.80E-01	2	Unchanged Medium
O14896	K05ef6	interferon regulatory factor 6	495.9782	951	406.9438	617.9736	-2.85E-01	9.39E-01	2	Unchanged Medium
G13ef5		interferon-gamma receptor (IFNG	616.4461	474	457.875	515.9592	-4.29E-01	-3.80E-01	2	Unchanged Medium
Q14116	L03ab6	interleukin 18 (interferon-gamma	1525.444	1610	556.9614	1230.533	-1.45E+00	7.71E-02	2	Unchanged Medium
O75874	H11ab7	isocitrate dehydrogenase 1 (NAC	660.9773	496	904.897	587.2716	4.53E-01	-4.14E-01	2	Unchanged Medium
PS1553	I21gh1	isocitrate dehydrogenase 3 (NAC	815.5318	899	784.1063	832.7908	-5.67E-02	1.40E-01	2	Unchanged Medium
P41252	P23ab6	isoleucine-tRNA synthetase	643.6728	316	992.267	650.6946	6.24E-01	-1.03E+00	2	Unchanged Medium
Q9UE99	J07ef7	Jagged 2	657.9935	460	656.5019	604.7722	8.21E-02	-5.17E-01	2	Unchanged Medium
PS2292	J14ab6	karyopherin alpha 2 (RAG cohort)	1105.911	1270	1670.406	1350.126	5.95E-01	2.04E-01	2	Unchanged Medium
P24390	E07cd7	KDEL (Lys-Asp-Glu-Leu) endopeptid	1556.771	1210	1411.383	1392.342	-1.41E-01	-3.65E-01	2	Unchanged Medium
P08779	L03ab7	keratin 16 (focal non-epidermolyt	815.5106	788	663.0228	754.7055	-2.99E-01	-5.39E-02	2	Unchanged Medium
Q04695	O24ab6	keratin 17	580.3123	1180	1056.274	937.1959	6.84E-01	1.02E+00	2	Unchanged Medium
Q07666	B04cd6	KH domain containing; RNA bind	1212.816	780	1103.092	1031.926	-1.37E-01	-6.37E-01	2	Unchanged Medium
Q14165	O16gh1	KIAA0152 gene product	285.0232	348	1374.81	669.3755	2.27E+00	2.89E-01	2	Unchanged Medium
Q12765	F03gh1	KIAA0193 gene product	951.658	1000	981.6527	979.0013	4.48E-02	7.68E-02	2	Unchanged Medium
Q43310	F11gh1	KIAA0427 gene product	482.1741	589	556.0999	542.3144	2.06E-01	2.88E-01	2	Unchanged Medium
Q43167	J03gh1	KIAA0441 gene product	1398.244	982	1102.589	1160.899	-3.43E-01	-5.10E-01	2	Unchanged Medium
Q9H7D5	H18gh7	KIAA1191 protein	886.4026	1930	1061.302	1291.483	2.60E-01	1.12E+00	2	Unchanged Medium
Q9HD96	L03cd8	LAG1 longevity assurance homolog	1319.272	798	1016.473	1044.592	-3.76E-01	-7.25E-01	2	Unchanged Medium
O00182	P04ab6	leclin; galactoside-binding; solub	760.6622	1300	527.6081	864.4149	-5.28E-01	7.79E-01	2	Unchanged Medium
Q99538	B04ef7	legumain	464.5	517	1105.037	695.3901	1.25E+01	1.53E-01	2	Unchanged Medium
Q95751	G01cd8	leucine zipper; down-regulated by	874.8344	274	970.9239	706.7407	1.50E-01	-1.67E+00	2	Unchanged Medium
O15468	P03cd4	lymphocyte immunoglobulin-like re	826.8073	939	1120.204	962.0679	4.36E-01	1.84E-01	2	Unchanged Medium
Q9UB84	I06cd8	likely mouse brain protein E46	877.3997	623	692.5911	731.0054	-3.41E-01	-4.94E-01	2	Unchanged Medium
Q9UFW4	N17ef8	likely ortholog of rat golgi stackin	1680.361	1700	2121.05	1834.238	3.36E-01	1.79E-02	2	Unchanged Medium
Q14847	P09ab7	LIM and SH3 protein 1	664.6143	758	895.1972	772.769	4.30E-01	1.91E-01	2	Unchanged Medium
O00158	M09ef3	LIM domain only 4	457.4088	299	1353.355	703.0924	1.56E+00	-6.16E-01	2	Unchanged Medium
Q9HAP6	M16gh5	LIN-7b protein; likely ortholog of t	2114.229	1550	2175.236	1945.862	4.10E-02	-4.50E-01	2	Unchanged Medium
P38571	K08ab6	lipase A; lysosomal acid; cholest	604.0401	587	512.8879	568.1283	-2.36E-01	-4.02E-02	2	Unchanged Medium
Q99732	H18cd5	LIPS-induced TNF-alpha factor	680.3876	893	449.4711	674.31	-5.98E-01	3.92E-01	2	Unchanged Medium
Q9V4Z1	O21ef4	Lsm3 protein	1641.224	1300	1596.905	1511.517	-3.85E-02	-3.40E-01	2	Unchanged Medium
O75895	D05cd7	lung cancer candidate	690.6061	772	601.3296	688.0098	-2.00E-01	1.61E-01	2	Unchanged Medium
Q06843	O07ef6	lymphotoxin beta (TNF superfam	405.7368	1040	298.9254	582.7217	-4.41E-01	1.36E+00	2	Unchanged Medium
Q95372	J04ef7	lysophospholipase II	480.0562	737	752.7079	656.485	6.49E-01	6.18E-01	2	Unchanged Medium
P13473	N06ab6	lysosomal-associated membrane	952.6393	2000	1277.773	1408.92	4.24E-01	1.07E+00	2	Unchanged Medium
Q08397	F09ab7	lysyl oxidase-like 1	1391.453	1633	2243.025	1753.531	6.89E-01	2.25E-01	2	Unchanged Medium
Q15046	B17ab7	lysyl-tRNA synthetase	900.8177	556	539.813	665.5485	-7.39E-01	-6.96E-01	2	Unchanged Medium
Q13312	D17cd3	MAD1 mitotic arrest deficient-like	807.7267	503	574.4266	628.231	-4.92E-01	-6.85E-01	2	Unchanged Medium
Q09160	A05ab6	major histocompatibility complex;	1524.076	2710	1290.783	1841.106	-2.40E-01	8.30E-01	2	Unchanged Medium
P40925	J23ab7	malate dehydrogenase 1; NAD (s	1144.218	788	1089.134	1007.157	-7.12E-02	-5.38E-01	2	Unchanged Medium
P40926	L01ab7	malate dehydrogenase 2; NAD (r	1525.837	1020	1212.544	1251.158	-3.32E-01	-5.88E-01	2	Unchanged Medium
Q16625	J15ef3	male-enhanced antigen	1253.21	1530	1827.301	1536.52	5.44E-01	2.87E-01	2	Unchanged Medium
Q9NQG1	C06gh5	mannosidase; beta A; lysosomal	533.2883	800	736.627	689.9075	4.66E-01	5.85E-01	2	Unchanged Medium
P26572	G11ab7	mannosyl (alpha-1,3)-glycoprot	619.6733	369	887.6535	625.3732	5.18E-01	-7.49E-01	2	Unchanged Medium
Q10469	G15ab7	mannosyl (alpha-1,6)-glycoprote	600.1049	583	636.621	606.4146	8.52E-02	-4.29E-02	2	Unchanged Medium
P41223	L09cd4	maternal G10 transcript	372.2443	563	575.7695	503.5179	6.29E-01	5.96E-01	2	Unchanged Medium
Q9V5V3	G13cd6	melanoma antigen; family D; 1	397.4495	952	1674.881	1008.268	2.08E+00	1.26E+00	2	Unchanged Medium
P43121	I22ef5	melanoma cell adhesion molecule	886.0756	795	432.1718	704.4837	-1.04E-01	-1.56E-01	2	Unchanged Medium
Q92494	D11ef1	membrane cofactor protein (CD4	737.352	1050	834.044	952.9144	-2.23E-01	1.11E-01	2	Unchanged Medium
Q14444	H15ab7	membrane component; chromost	549.4803	666	464.8174	560.0583	-2.41E-01	2.77E-01	2	Unchanged Medium
Q9NPE2	O12ef2	mesenchymal stem cell protein C	749.8838	932	1065.26	922.5469	5.33E-01	3.14E-01	2	Unchanged Medium
Q92571	G07ab7	mesoderm specific transcript hon	617.581	446	537.1735	533.4868	-2.01E-01	-4.71E-01	2	Unchanged Medium
Q95204	N11ef3	metalloprotease 1 (pltrifysin famil	735.157	349	478.8153	520.899	-6.19E-01	-1.08E+00	2	Unchanged Medium
P80297	H20ab7	metallothionein 1L	589.6327	502	656.4441	562.747	1.55E-01	-2.32E-01	2	Unchanged Medium
Q99735	C18ef7	microsomal glutathione S-transfer	527.4698	686	373.9779	529.1741	-4.98E-01	3.79E-01	2	Unchanged Medium
Q98XW5	D13gh8	microtubule-associated protein 1	247.2817	692	887.8299	609.0447	1.84E+00	1.49E+00	2	Unchanged Medium
Q9Y6C9	M14ef3	mitochondrial carrier homolog 2	1874.893	1910	1893.062	1892.145	1.39E-02	2.56E-02	2	Unchanged Medium
Q9v387	E07ef2	mitochondrial ribosomal protein L	401.0368	421	732.113	517.9208	8.68E-01	6.88E-02	2	Unchanged Medium
Q9P015	A12ef8	mitochondrial ribosomal protein L	553.658	760	589.0617	634.2498	8.94E-02	4.57E-01	2	Unchanged Medium
Q9NWX0	M06gh2	mitochondrial ribosomal protein L	642.9143	496	701.1442	613.4293	1.25E-01	-3.74E-01	2	Unchanged Medium
Q9H0U6	O13ef8	mitochondrial ribosomal protein L	741.5383	1000	826.8818	856.3674	1.57E-01	4.32E-01	2	Unchanged Medium
Q9NZE8	O04ef2	mitochondrial ribosomal protein L	914.9722	910	956.7888	927.2731	6.45E-02	-7.77E-03	2	Unchanged Medium
Q9P0P3	K18ef2	mitochondrial ribosomal protein L	1217.101	891	1195.143	1101.306	-2.51E-02	-4.50E-01	2	Unchanged Medium
Q9Y317	M15ef2	mitochondrial ribosomal protein L	799.6979	1020	1372.352	1063.499	7.79E-01	3.49E-01	2	Unchanged Medium
Q9Y6G3	C19ef8	mitochondrial ribosomal protein L	571.7264	810	689.3229	690.2211	2.70E-01	5.02E-01	2	Unchanged Medium

Q9BYC7	K12gh8	mitochondrial ribosomal protein L	490.5463	655	619.0928	591.6118	3.36E-01	4.39E-01	2	Unchanged Medium
Q9Y3D3	B12ef1	mitochondrial ribosomal protein S	966.7611	1020	1006.958	897.1495	5.88E-02	7.41E-02	2	Unchanged Medium
Q9Y6T6	C15ef8	mitochondrial ribosomal protein S	683.2889	580	761.9887	674.9976	1.57E-01	-2.37E-01	2	Unchanged Medium
Q9Y3D5	G19ef2	mitochondrial ribosomal protein S	696.3306	1080	825.5557	865.8021	2.46E-01	6.27E-01	2	Unchanged Medium
P82921	O11gh7	mitochondrial ribosomal protein S	748.082	1190	1115.5	1019.33	5.76E-01	6.75E-01	2	Unchanged Medium
P82650	D07gh4	mitochondrial ribosomal protein S	554.1784	515	470.683	513.1921	-2.36E-01	-1.07E-01	2	Unchanged Medium
Q9Y2Q9	A03ef8	mitochondrial ribosomal protein S	1439.076	1420	1329.749	1395.534	-1.14E-01	-2.15E-02	2	Unchanged Medium
Q9NP92	F02ef3	mitochondrial ribosomal protein S	669.1652	532	617.3223	606.105	-1.16E-01	-3.31E-01	2	Unchanged Medium
Q02750	J08ef5	mitogen-activated protein kinase	615.689	701	453.8702	590.1129	-4.40E-01	1.87E-01	2	Unchanged Medium
Q02779	K09ab7	mitogen-activated protein kinase	597.1743	423	509.6637	510.095	-2.29E-01	-4.96E-01	2	Unchanged Medium
Q12851	N10ab8	mitogen-activated protein kinase	988.0971	1020	976.7391	994.1804	-1.67E-02	4.26E-02	2	Unchanged Medium
P49137	J06ef5	mitogen-activated protein kinase	942.7459	1000	1068.579	1004.624	1.81E-01	8.87E-02	2	Unchanged Medium
Q9BYG3	O02gh8	MK167 (FHA domain) interacting	791.8688	407	307.4404	502.0002	-1.36E+00	-9.61E-01	2	Unchanged Medium
Q15014	C17cd8	MORF-related gene X	1146.48	1030	1262.273	1144.777	1.39E-01	-1.61E-01	2	Unchanged Medium
	F22ef4	mRNA: clone:PO2ST9	1052.442	1040	905.2614	999.5166	-2.17E-01	-1.60E-02	2	Unchanged Medium
Q15773	M18ef5	myeloid leukemia factor 2	577.4585	467	766.6809	603.749	4.09E-01	-3.06E-01	2	Unchanged Medium
P35579	O01ef1	myostin; heavy polypeptide 9; nor	1426.003	1150	1203.964	1281.007	-2.44E-01	-3.07E-01	2	Unchanged Medium
Q9Y6D2	C21ef2	N-acetyltransferase 5 (ARD1 homolog)	531.5485	708	274.971	504.9319	-9.51E-01	4.14E-01	2	Unchanged Medium
P41227	G13gh1	N-acetyltransferase; homolog of	800.6676	905	818.2554	841.2057	3.13E-02	1.76E-01	2	Unchanged Medium
Q13510	H20ab2	N-acylsphingosine amidohydrolase	752.1534	1660	877.5006	1028.456	-1.51E-01	1.14E+00	2	Unchanged Medium
Q43678	O09ab7	NADH dehydrogenase (ubiquinol)	1366.754	1930	2137.906	1810.699	6.45E-01	4.96E-01	2	Unchanged Medium
Q95167	E24ab7	NADH dehydrogenase (ubiquinol)	1431.655	1770	1506.934	1570.238	7.39E-02	3.08E-01	2	Unchanged Medium
P56556	O11ab7	NADH dehydrogenase (ubiquinol)	1650.612	916	795.8725	1120.973	-1.05E+00	-8.49E-01	2	Unchanged Medium
Q95182	K06ab7	NADH dehydrogenase (ubiquinol)	750.0893	777	725.1711	750.6457	-4.87E-02	5.03E-02	2	Unchanged Medium
P51970	L04cd8	NADH dehydrogenase (ubiquinol)	554.1995	728	1021.163	767.6928	8.82E-01	3.93E-01	2	Unchanged Medium
Q96000	J10ab8	NADH dehydrogenase (ubiquinol)	1110.197	1440	1111.615	1219.158	1.84E-03	3.71E-01	2	Unchanged Medium
Q95178	J06ab8	NADH dehydrogenase (ubiquinol)	925.3926	758	815.266	836.3224	-1.63E-01	-2.68E-01	2	Unchanged Medium
Q95139	M03ab8	NADH dehydrogenase (ubiquinol)	1392.873	1480	2162.279	1678.472	6.34E-01	8.78E-02	2	Unchanged Medium
P17568	H02ab8	NADH dehydrogenase (ubiquinol)	787.0681	567	591.1924	648.3703	-4.13E-01	-4.74E-01	2	Unchanged Medium
Q9Y6M9	P16ab8	NADH dehydrogenase (ubiquinol)	1299.803	1450	746.8017	1184.524	-7.99E-01	1.55E-01	2	Unchanged Medium
Q43677	M05ab8	NADH dehydrogenase (ubiquinol)	586.5059	601	532.551	573.2205	-1.39E-01	3.43E-02	2	Unchanged Medium
Q00217	M09ab8	NADH dehydrogenase (ubiquinol)	1383.411	1130	1194.001	1234.615	-2.12E-01	-2.96E-01	2	Unchanged Medium
P19404	M07ef1	NADH dehydrogenase (ubiquinol)	1151.224	443	356.308	650.0945	-1.69E+00	-1.36E+00	2	Unchanged Medium
Q76008	A12cd6	Nef-associated factor 1	720.2744	951	424.04	698.4474	-7.64E-01	4.01E-01	2	Unchanged Medium
Q9UPY4	K22ef3	nesca protein	425.9149	459	621.9336	505.6782	5.46E-01	1.40E-01	2	Unchanged Medium
	L19gh8	neurabin II	1241.544	862	1023.077	1042.081	-2.79E-01	-5.27E-01	2	Unchanged Medium
Q99742	O07ab8	neuronal PAS domain protein 1	1076.259	405	605.3589	695.8521	-8.28E-01	-1.41E+00	2	Unchanged Medium
Q50448	P20ef3	neuronal thread protein	1831.592	1650	1490.624	1662.051	-2.97E-01	-1.38E-01	2	Unchanged Medium
Q9UNW9	O05ab8	neuro-oncological ventral antigen	1049.959	1050	1219.792	1106.982	2.16E-01	1.70E-03	2	Unchanged Medium
Q9UGL9	C09gh3	NICE-1 protein	1026.838	1380	381.058	923.3423	-1.43E+00	-4.08E-01	2	Unchanged Medium
Q9UGL6	M09ef4	NICE-5 protein	912.7542	1390	955.016	1086.502	6.53E-02	6.09E-01	2	Unchanged Medium
Q92982	I09ef7	ninjurin 1	458.23	689	412.0181	519.6852	-1.53E-01	5.88E-01	2	Unchanged Medium
Q9BPW8	N19cd3	nipsnap homolog 1 (C. elegans)	829.4266	529	562.9689	640.3075	-5.59E-01	-8.50E-01	2	Unchanged Medium
Q9NQR4	B13gh4	Nit protein 2	519.1587	868	665.8632	684.4701	3.59E-01	7.42E-01	2	Unchanged Medium
Q9UF10	L08ef2	non-canonical ubiquitin conjugate	1336.406	2000	1488.008	1608.811	1.55E-01	5.83E-01	2	Unchanged Medium
Q9Y385	H11ef2	non-canonical ubiquitin conjugate	625.6356	808	669.812	701.1992	9.84E-02	3.69E-01	2	Unchanged Medium
Q15233	O02ef1	non-POU domain containing; oct	1083.363	1210	1234.216	1174.503	1.88E-01	1.55E-01	2	Unchanged Medium
Q13137	A03cd6	nuclear domain 10 protein	910.7725	914	94.6079	923.1712	5.26E-02	5.31E-03	2	Unchanged Medium
Q16236	M03cd1	nuclear factor (erythroid-derived	1233.751	1180	1043.638	1153.088	-2.41E-01	-6.20E-02	2	Unchanged Medium
P08651	B07ef2	nuclear factor I/C (CCAAT-binding	726.0476	624	659.6305	669.8575	-1.38E-01	-2.19E-01	2	Unchanged Medium
Q95134	P10cd3	nuclear localization signal delete	465.2933	522	536.7333	508.0938	2.06E-01	1.87E-01	2	Unchanged Medium
Q15772	N19ab2	nuclear protein; marker for differ	1473.704	923	1157.202	1184.738	-3.49E-01	-6.75E-01	2	Unchanged Medium
Q9UHY1	L15cd8	nuclear receptor binding protein	515.949	948	619.7512	694.4539	2.64E-01	8.77E-01	2	Unchanged Medium
Q9UPC9	H23ab2	nuclear receptor coactivator 3	822.7768	1190	932.9058	982.77	1.81E-01	5.36E-01	2	Unchanged Medium
Q15325	N22cd2	nuclease sensitive element bindi	1644.614	1720	2064.24	1808.771	3.28E-01	6.25E-02	2	Unchanged Medium
P00567	D05cd6	nucleolar protein 5A (56kD with H	659.4335	608	623.2536	630.2325	-8.14E-02	-1.17E-01	2	Unchanged Medium
Q9NX24	A10gh3	nucleolar protein family A; memb	466.2539	625	594.8443	561.9547	3.51E-01	4.22E-01	2	Unchanged Medium
P06748	K08gh6	nucleophosphin (nucleolar phosph	1605.368	1080	1136.972	1275.358	-4.98E-01	-5.87E-01	2	Unchanged Medium
P50583	B01ab2	nudix (nucleoside diphosphate li	1590.763	211	251.3768	684.354	-2.66E+00	-2.91E+00	2	Unchanged Medium
Q9UHM6	N20gh8	opsin 4 (melanopsin)	1076.73	1200	1643.887	1305.239	6.10E-01	1.50E-01	2	Unchanged Medium
Q9Y218	P22gh1	optineurin	1014.697	1980	912.1917	1302.823	-1.54E-01	9.65E-01	2	Unchanged Medium
Q16612	O01cd5	P311 protein	322.7444	349	223.8416	967.7934	2.79E+00	1.12E-01	2	Unchanged Medium
P55771	J21cd7	paired box gene 9	692.506	380	573.135	548.4374	-2.73E-01	-8.67E-01	2	Unchanged Medium
Q9UKJ1	N21cd8	paired immunoglobulin-like recep	674.1862	450	558.3225	560.9087	-2.72E-01	-5.83E-01	2	Unchanged Medium
Q15165	P24ab7	paraoxonase 2	338.5244	891	563.7771	604.4337	7.86E-01	1.40E+00	2	Unchanged Medium
Q7002	P06ef5	PCTAIRE protein kinase 3	836.5659	916	632.7298	795.1858	-4.03E-01	1.31E-01	2	Unchanged Medium
Q9Y3C8	J07ef2	peptidyl-prolyl Isomerase (cydop)	548.5938	731	26.6097	602.0621	-5.90E-02	4.14E-01	2	Unchanged Medium
P30405	F14cd5	peptidyl-prolyl Isomerase F (cydo	843.1834	925	467.6738	745.2396	-8.50E-01	1.33E-01	2	Unchanged Medium
Q43924	G24ab8	phosphodiesterase 6D; cGMP-er	373.1208	630	699.1887	567.4949	9.06E-01	7.56E-01	2	Unchanged Medium
P17858	K10ab8	phosphofructokinase; liver	950.5746	525	774.727	750.1835	-2.95E-01	-8.56E-01	2	Unchanged Medium
Q01813	C17ef1	phosphofructokinase; platelet	573.5211	646	555.9236	591.6879	-4.50E-02	1.71E-01	2	Unchanged Medium
Q00511	N20cd3	phosphoprotein enriched in astro	1330.005	1500	2288.098	1704.656	7.83E-01	1.70E-01	2	Unchanged Medium
P11216	B16ab8	phosphorylase; glycogen; brain	516.7984	495	988.163	666.5476	9.35E-01	-6.30E-02	2	Unchanged Medium
P00749	P19ef7	plasm/arginen activator; urokinase	1096.052	3440	1051.513	1861.568	-5.98E-02	1.65E+00	2	Unchanged Medium
P13797	C13cd1	plaslin 3 (T Isoform)	990.1173	804	1393.037	1062.438	4.93E-01	-3.00E-01	2	Unchanged Medium
Q15102	E16ab8	platelet-activating factor acetylhy	469.9778	674	468.9765	537.6872	-3.08E-03	5.20E-01	2	Unchanged Medium
P01127	A08ef5	platelet-derived growth factor bet	500.6466	674	456.4576	543.5869	-1.33E-01	4.28E-01	2	Unchanged Medium
Q15795	C19ef6	pleckstrin homology; Sec7 and c	578.295	740	518.8327	612.22	-1.57E-01	3.55E-01	2	Unchanged Medium
Q43660	O18ab8	pielo tropic regulator 1 (PRL1hor	743.7263	933	804.3456	827.0995	1.13E-01	3.27E-01	2	Unchanged Medium
Q15155	G12ef3	pM5 protein	664.2511	423	490.295	525.8869	-4.38E-01	-6.51E-01	2	Unchanged Medium
Q9H361	L04gh7	poly(A) binding protein; cytoplas	759.4566	491	710.9543	653.8286	-9.52E-02	-8.29E-01	2	Unchanged Medium
Q15366	A11cd1	poly(rC) binding protein 2	1951.241	1490	2128.585	1857.745	1.26E-01	-3.86E-01	2	Unchanged Medium
P19388	B15ab8	polymerase (RNA) II (DNA direct	552.3545	529	698.4965	593.4201	3.39E-01	-6.12E-02	2	Unchanged Medium
P52434	F05gh6	polymerase (RNA) II (DNA direct	949.7064	1480	1210.411	1211.761	3.50E-01	6.35E-01	2	Unchanged Medium
P36954	A20cd1	polymerase (RNA) II (DNA direct	1603.557	1820	1413.573	1613.004	-1.82E-01	1.84E-01	2	Unchanged Medium
P53803	C17cd1	polymerase (RNA) II (DNA direct	437.9544	893	528.0144	619.8184	2.70E-01	1.03E+00	2	Unchanged Medium

Q9UQQ3	J08cd6	POP4 (processing of precursor ; postmoltic segregation increase	480.5848	645	551.3661	558.9966	1.98E-01	4.25E-01	2	Unchanged Medium
Q13670	B07ab8	potassium channel modulatory fa	812.7865	779	532.0548	708.0473	-6.11E-01	-6.07E-02	2	Unchanged Medium
Q5P0J7	L07gh4	potassium channel modulatory fa	1401.591	1720	1192.2024	1438.482	-2.33E-01	2.97E-01	2	Unchanged Medium
O60925	K02ab8	prefoldin 1	1631.996	1720	1860.632	1737.289	1.89E-01	7.51E-02	2	Unchanged Medium
Q9UHV9	J15ef4	prefoldin 2	514.4897	882	833.1525	743.3158	6.95E-01	7.78E-01	2	Unchanged Medium
Q13519	J07ef5	prepronocleptin	564.2079	464	887.4522	638.4071	6.53E-01	-2.83E-01	2	Unchanged Medium
P04156	A13ab8	prion protein (p27-30) (Creutzfeldt	797.9495	631	701.8217	710.1438	-1.85E-01	-3.39E-01	2	Unchanged Medium
Q9UJ73	K03ef8	PRO0246 protein	430.412	535	546.8599	504.0018	3.45E-01	3.13E-01	2	Unchanged Medium
Q5P0T3	D14ef1	proapoptotic caspase adaptor pn	1261.463	1650	2553.652	1820.221	1.02E+00	3.83E-01	2	Unchanged Medium
Q02809	P20ab7	procollagen-lysine; 2-oxoglutarate	503.7557	477	1993.232	991.2271	1.98E+00	-7.97E-02	2	Unchanged Medium
P07237	G13ab8	procollagen-proline; 2-oxoglutarate	633.8309	406	575.6635	538.3489	-1.39E-01	-6.44E-01	2	Unchanged Medium
P09466	E12ab8	progesterone-associated endome	367.0939	625	708.8717	567.0247	9.49E-01	7.68E-01	2	Unchanged Medium
Q16342	G22ef6	programmed cell death 2	735.0961	759	490.3938	661.3332	-5.84E-01	4.52E-02	2	Unchanged Medium
O75340	I02cd8	programmed cell death 6	1055.886	1090	1356.597	1167.782	3.82E-01	4.70E-02	2	Unchanged Medium
P35232	C22ef5	prohibitin	2045.693	1810	1600.236	1818.121	-3.54E-01	-1.78E-01	2	Unchanged Medium
Q9UQ80	O03cd1	proliferation-associated 2G4; 3B	1902.387	1390	2003.135	1763.59	7.44E-02	-4.58E-01	2	Unchanged Medium
Q12796	E05ab3	proline rich 2	1927.78	1530	1475.973	1643.691	-3.85E-01	-3.36E-01	2	Unchanged Medium
Q15168	P20cd2	proline-rich protein BstNI subfamily	997.5582	1290	1404.4	1232.034	4.93E-01	3.76E-01	2	Unchanged Medium
P35998	L09ab8	proteasome (prosome; macropal	1010.463	1200	1059.594	1090.401	6.85E-02	2.49E-01	2	Unchanged Medium
P47210	N16cd2	proteasome (prosome; macropal	1037.339	1150	1193	1127.918	2.02E-01	1.53E-01	2	Unchanged Medium
O00495	N03ab8	proteasome (prosome; macropal	1043.875	498	563.7775	701.7628	-8.89E-01	-1.07E+00	2	Unchanged Medium
O75831	N07ab8	proteasome (prosome; macropal	763.7632	622	506.8297	630.7237	-5.92E-01	-2.97E-01	2	Unchanged Medium
Q13200	L15ab8	proteasome (prosome; macropal	644.3008	594	331.4288	523.3702	-9.59E-01	-1.16E-01	2	Unchanged Medium
O43242	L17ab8	proteasome (prosome; macropal	2159.327	1230	1637.67	1675.386	-3.99E-01	-8.13E-01	2	Unchanged Medium
P55036	N18cd2	proteasome (prosome; macropal	460.8093	724	588.5346	591.0419	3.53E-01	6.51E-01	2	Unchanged Medium
P48556	L21ab8	proteasome (prosome; macropal	1240.243	1030	1885.116	1317.42	4.42E-01	-2.72E-01	2	Unchanged Medium
Q52530	G07cd6	proteasome (prosome; macropal	1804.777	1570	1800.731	1724.253	-3.24E-03	-2.04E-01	2	Unchanged Medium
P28066	J13ab8	proteasome (prosome; macropal	766.589	767	775.2704	769.7417	1.62E-02	1.46E-03	2	Unchanged Medium
O14818	J15ab8	proteasome (prosome; macropal	1242.517	1540	1139.994	1308.162	-1.24E-01	3.12E-01	2	Unchanged Medium
P49721	J19ab8	proteasome (prosome; macropal	1832.921	2110	1817.062	1853.89	-1.81E-01	2.04E-01	2	Unchanged Medium
P28062	H18ab8	proteasome (prosome; macropal	797.3912	905	505.3368	735.864	-6.58E-01	1.82E-01	2	Unchanged Medium
P28065	B06ef7	proteasome (prosome; macropal	771.1998	1630	1002.72	1133.626	3.79E-01	1.08E+00	2	Unchanged Medium
P10619	A07ab8	protective protein for beta-galact	1539.157	907	980.3046	1142.279	-6.51E-01	-7.62E-01	2	Unchanged Medium
Q9UNN8	F03cd6	protein C receptor; endothelial (E	892.1589	702	488.5084	694.2014	-8.69E-01	-3.46E-01	2	Unchanged Medium
Q15084	H02cd5	protein disulfide isomerase-relat	1081.309	407	859.0228	762.4339	-3.32E-01	-1.41E+00	2	Unchanged Medium
Q9Y289	C22cd7	protein kinase (cAMP-dependent	650.9588	1040	754.6101	814.4047	2.13E-01	6.73E-01	2	Unchanged Medium
Q13517	A09ef5	protein kinase C binding protein	380.9448	587	630.5497	532.9442	7.27E-01	6.25E-01	2	Unchanged Medium
P54619	F15ab8	protein kinase; AMP-activated; g	482.8359	572	841.1746	632.0378	8.01E-01	2.45E-01	2	Unchanged Medium
P17612	F13ab8	protein kinase; cAMP-dependent	643.0385	629	901.5293	724.5168	4.87E-01	-3.19E-02	2	Unchanged Medium
P09131	F10gh1	Protein P3	529.0069	607	617.0621	584.2407	2.22E-01	1.98E-01	2	Unchanged Medium
O60927	P02gh1	protein phosphatase 1; regulator	1728.646	1760	1404.955	1630.486	-2.99E-01	2.42E-02	2	Unchanged Medium
P41236	C08cd1	protein phosphatase 1; regulator	532.1136	621	583.7663	578.9436	1.34E-01	2.23E-01	2	Unchanged Medium
Q15435	M15ab8	protein phosphatase 1; regulator	634.9759	963	753.9046	784.0242	2.48E-01	6.01E-01	2	Unchanged Medium
P05323	E13ef6	protein phosphatase 2 (formerly : 1058.276	1120	796.6526	992.192	-4.10E-01	8.39E-02	2	Unchanged Medium	
Q15257	G01ef5	protein phosphatase 2A; regulator	925.4458	905	1160.437	996.8116	3.26E-01	-3.29E-02	2	Unchanged Medium
P33172	F01ab8	protein phosphatase 4 (formerly : 1791.171	1220	1064.665	137.256	-7.51E-01	-5.59E-01	2	Unchanged Medium	
O00743	F03ab8	protein phosphatase 6; catalytic :	998.7	1070	738.4815	936.2693	-4.35E-01	1.02E-01	2	Unchanged Medium
P38391	E21cd7	protein translocational complex be	1049.306	1050	1428.451	1175.447	4.45E-01	-9.93E-04	2	Unchanged Medium
P78324	M17cd4	protein tyrosine phosphatase; no	639.2381	741	591.4877	657.1953	-1.12E-01	2.13E-01	2	Unchanged Medium
Q13332	P21ab8	protein tyrosine phosphatase; ret	1882.284	1880	2019.865	1928.827	1.02E-01	1.57E-03	2	Unchanged Medium
Q9HA06	C08gh6	protoactinidin 16 dachshous-like (	967.2552	906	1070.494	981.1143	1.48E-01	-9.50E-02	2	Unchanged Medium
O43445	E11cd5	PPR4 pre-mRNA processing fact	777.1081	549	569.3749	631.8368	-4.49E-01	-5.01E-01	2	Unchanged Medium
Q9Y6B3	L19ef2	PTD013 protein	652.1251	701	1031.739	794.9108	6.62E-01	1.04E-01	2	Unchanged Medium
Q9HAN1	P19gh6	pumilio homolog 1 ( <i>Drosophila</i> )	842.4925	1170	1047.18	1019.213	3.14E-01	4.71E-01	2	Unchanged Medium
Q9NQA4	C23ef4	putative acid-sensing ion channe	742.723	762	678.3813	727.7123	-1.31E-01	3.70E-02	2	Unchanged Medium
O43598	J05cd6	putative c-Myc-responsive	473.6498	621	459.383	517.9666	-4.41E-02	3.90E-01	2	Unchanged Medium
O43257	M12cd6	putative cyclin G1 Interacting pro	1118.374	1190	1238.925	1183.655	1.48E-01	9.40E-02	2	Unchanged Medium
Q9NY06	M07ef4	putative integral membrane trans	966.4384	544	569.8585	693.4947	-7.62E-01	-8.29E-01	2	Unchanged Medium
P17152	H21cd4	putative receptor protein	399.8305	650	591.3162	547.0229	5.64E-01	7.00E-01	2	Unchanged Medium
Q9Y619	B13ef2	putative secreted protein	373.307	485	742.5337	533.7168	9.92E-01	3.79E-01	2	Unchanged Medium
P54886	B12ab8	pyrrolidine-5-carboxylate synthet	406.7128	302	905.8993	538.0842	1.16E+00	-4.31E-01	2	Unchanged Medium
Q13876	B03ef7	quiescin Q6	745.299	585	824.2489	718.0657	1.45E-01	-3.50E-01	2	Unchanged Medium
O14679	K24ef5	quinone oxidoreductase homolog	710.5753	1160	651.2257	839.1208	-1.26E-01	7.02E-01	2	Unchanged Medium
P53611	N16ab8	Rab geranylgeranyltransferase; I	758.1496	727	938.6179	807.7755	3.08E-01	-6.14E-02	2	Unchanged Medium
P47224	D06ab8	RAB interacting factor	645.5902	859	577.3956	693.8748	-1.61E-01	4.11E-01	2	Unchanged Medium
Q15907	H04cd4	RAB18; member RAS oncogene	926.8757	1030	1224.758	1060.693	4.02E-01	1.53E-01	2	Unchanged Medium
P51153	D04ab8	RAB13; member RAS oncogene	619.0867	935	1131.86	895.2783	8.70E-01	5.95E-01	2	Unchanged Medium
P35287	J24ef2	RAB14; member RAS oncogene	543.7425	584	586.1635	571.2023	1.08E-01	1.02E-01	2	Unchanged Medium
Q9NP72	P02ef8	RAB18; member RAS oncogene	459.4786	794	834.6616	629.3713	4.66E-01	7.89E-01	2	Unchanged Medium
P11476	H22ab8	RAB1A; member RAS oncogene	1039.455	767	993.586	933.4801	-6.51E-01	-4.38E-01	2	Unchanged Medium
Q9H0U4	L08gh7	RAB1B; member RAS oncogene	526.9862	691	696.5292	638.0939	4.02E-01	3.90E-01	2	Unchanged Medium
P08886	B22ab8	RAB2; member RAS oncogene	1483.703	1900	2195.304	1658.384	5.65E-01	3.54E-01	2	Unchanged Medium
O95716	P04cd4	RAB3D; member RAS oncogene	908.9015	638	556.2242	701.161	-7.08E-01	-5.10E-01	2	Unchanged Medium
P35239	D02ab8	RAB5B; member RAS oncogene	598.5113	708	393.3892	566.5496	-6.05E-01	2.42E-01	2	Unchanged Medium
P20340	C07ef6	RAB6A; member RAS oncogene	503.1507	655	416.7552	524.9788	-2.72E-01	3.81E-01	2	Unchanged Medium
P43497	D16ab8	RAN binding protein 1	1438.305	1180	1786.177	1468.585	3.13E-01	-2.84E-01	2	Unchanged Medium
Q9U126	B20ef1	Ran binding protein 11	1505.224	1180	1273.677	1319.368	-2.41E-01	-3.52E-01	2	Unchanged Medium
P47736	D18ab8	RAP1; GTPase activating prote	875.8692	414	461.3322	563.6391	-9.25E-01	-1.08E+00	2	Unchanged Medium
Q15382	F17cd2	Ras homolog enriched in brain 2	1435.587	2190	1635.792	1754.23	1.88E-01	6.10E-01	2	Unchanged Medium
P52199	B18ab2	ras homolog gene family; membe	534.6169	1520	399.0517	816.6152	-4.22E-01	1.50E+00	2	Unchanged Medium
P35238	B20ab2	ras homolog gene family; membe	1022.646	872	1019.472	971.4616	-4.48E-03	-2.29E-01	2	Unchanged Medium
Q14644	J08ef7	RAS p21 protein activator (GTP <sub>a</sub> )	615.946	623	627.059	622.1475	2.58E-02	1.74E-02	2	Unchanged Medium
Q15404	A10cd8	Ras suppressor protein 1	1543.953	1920	2317.155	1925.544	5.86E-01	3.11E-01	2	Unchanged Medium
Q13283	H14cd5	Ras-GTPase-activating protein S	846.7267	789	571.1476	735.5498	-5.68E-01	-1.02E-01	2	Unchanged Medium
Q9NVQ9	M05gh1	Rec8p; a meiotic recombination	1334.371	1200	1325.85	1286.027	-9.24E-03	-1.56E-01	2	Unchanged Medium
O60895	K17cd6	receptor (calctonin) activity modi	572.8174	519	899.2606	663.6562	6.51E-01	-1.43E-01	2	Unchanged Medium

P35244	I22ef6	replication protein A3 (14kD)	544.0212	502	924.5385	656.7974	7.65E-01	-1.16E-01	2	Unchanged Medium
Q99623	D03cd7	repressor of estrogen receptor $\alpha$	1139.283	689	1233.151	1020.486	1.14E-01	-7.25E-01	2	Unchanged Medium
Q9UMQ4	C01gh1	ret proto-oncogene (multiple end)	769.2484	602	803.931	725.1999	6.35E-02	-3.53E-01	2	Unchanged Medium
Q9NQC3	M19cd7	reticulin 4	1459.586	586	927.976	991.1835	-6.53E-01	-1.32E+00	2	Unchanged Medium
P47804	P03cd1	retinal G protein coupled receptor	403.1219	497	627.4176	509.1489	6.38E-01	3.02E-01	2	Unchanged Medium
Q16576	P07ef6	retinoblastoma binding protein 7	1539.006	1410	798.8744	1250.347	-9.46E-01	-1.23E-01	2	Unchanged Medium
O95357	D02cd4	retinoic acid induced 3	678.1926	713	206.6352	532.4837	-1.71E+00	7.14E-02	2	Unchanged Medium
Q15299	D20ef1	retinoic acid receptor-beta assoc	1060.232	979	1013.444	1017.603	-6.51E-02	-1.15E-01	2	Unchanged Medium
Q9UUY1	P05ef2	retinoic acid repressible protein	610.5279	726	586.2413	841.044	-5.86E-02	-2.51E-01	2	Unchanged Medium
Q13017	M15ef8	Rho GTPase activating protein 5	560.443	807	514.6138	627.5049	-1.23E-01	5.27E-01	2	Unchanged Medium
Q43182	B24ab2	Rho GTPase activating protein 6	1257.146	806	895.7191	988.3979	-4.89E-01	-6.41E-01	2	Unchanged Medium
O60274	F04gh6	Rho-specific guanine nucleotide	651.9484	577	368.4761	531.8448	-8.31E-01	-1.76E-01	2	Unchanged Medium
P07998	P21cd1	ribonuclease; RNase A family; 1	1294.476	3040	1532.811	1976.991	2.99E-01	1.23E+00	2	Unchanged Medium
P04843	B12cd1	ribophorin I	1493.814	1360	2248.214	1700.316	5.90E-01	-1.37E-01	2	Unchanged Medium
P04844	B14cd1	ribophorin II	1574.181	1170	1880.047	1540.481	2.58E-01	-4.32E-01	2	Unchanged Medium
P26373	D11cd1	ribosomal protein L13	2091.256	1200	1924.546	1739.922	-1.20E-01	-7.97E-01	2	Unchanged Medium
P40429	H12ef1	ribosomal protein L13a	1928.024	2060	1091.46	1694.794	-8.21E-01	9.89E-02	2	Unchanged Medium
P39019	J05cd1	ribosomal protein S19	1794.844	1480	2253.771	1841.785	3.29E-01	-2.81E-01	2	Unchanged Medium
P78317	B04cd1	ring finger protein 4	756.2395	661	668.8027	695.4611	-1.77E-01	-1.93E-01	2	Unchanged Medium
Q99942	F04cd2	ring finger protein 5	1016.837	949	1126.187	1030.595	1.47E-01	-1.00E-01	2	Unchanged Medium
O43148	A15cd4	RNA (guanine-7- methyltransfer)	572.6495	730	390.498	564.3647	-5.52E-01	3.50E-01	2	Unchanged Medium
O02916	F06ab6	RNA binding motif protein 4	533.7121	628	430.5298	530.87	-3.10E-01	2.36E-01	2	Unchanged Medium
Q9Y580	J10gh6	RNA binding motif protein 7	368.8423	710	558.043	545.5838	5.97E-01	9.45E-01	2	Unchanged Medium
Q14621	H07cd7	RNA binding protein (autoantigen)	499.5699	737	508.822	581.142	2.08E-02	5.61E-01	2	Unchanged Medium
Q93062	K17cd7	RNA-binding protein gene with r	845.0994	859	640.4514	714.6837	-4.00E-01	-3.80E-01	2	Unchanged Medium
Q99497	B15cd7	RNA-binding protein regulatory s	1914.86	1400	2563.974	1958.111	4.21E-01	-4.56E-01	2	Unchanged Medium
Q99584	L17cd2	S100 calcium binding protein A1:	492.6196	421	675.1457	529.713	4.55E-01	-2.25E-01	2	Unchanged Medium
P23526	A06ef1	S-adenosylhomocysteine hydrol	550.6181	603	478.692	544.258	-2.02E-01	1.32E-01	2	Unchanged Medium
O43865	H21ab2	S-adenosylhomocysteine hydrol	1460.581	526	466.4887	817.8431	-1.65E+00	-1.47E+00	2	Unchanged Medium
O14828	D02cd5	secretory carrier membrane protein	661.3975	460	481.9262	534.3923	-4.57E-01	-5.24E-01	2	Unchanged Medium
O75326	L05cd3	semi domain; immunoglobulin d	795.0564	768	943.1132	635.2276	4.26E-01	-5.09E-02	2	Unchanged Medium
O43278	I16cd2	serine protease inhibitor; Kunitz I	1295.263	1260	641.0775	1066.162	-1.01E+00	-3.74E-02	2	Unchanged Medium
O00271	C05ef5	serine protease inhibitor; Kunitz I	1379.545	1740	876.4128	1332.552	-6.55E-01	3.36E-01	2	Unchanged Medium
Q9UEW8	N22ef5	serine/threonine kinase 39 (STE)	1230.117	1030	841.1872	1032.185	-5.48E-01	-2.63E-01	2	Unchanged Medium
Q13043	P15cd2	serine/threonine kinase 4	750.7132	838	756.1662	781.5546	1.04E-02	1.58E-01	2	Unchanged Medium
Q9Y282	F01ef2	serologically defined breast canc	1279.414	1160	1907.544	1448.986	5.76E-01	-1.41E-01	2	Unchanged Medium
P35542	A02gh1	serum amyloid A4; constitutive	754.5041	1310	811.5701	959.3499	1.05E-01	7.98E-01	2	Unchanged Medium
O75799	I22cd6	seven transmembrane domain pr	761.3872	778	799.0998	779.5745	6.97E-02	3.16E-02	2	Unchanged Medium
Q9P0V3	H17ef3	SH3-domain binding protein 4	1204.005	1710	1539.363	1483.624	3.54E-01	5.04E-01	2	Unchanged Medium
Q99519	C13ab8	slalidase 1 (lysosomal slalidase)	712.4593	680	498.7449	630.4428	-5.15E-01	-6.70E-02	2	Unchanged Medium
Q92185	J20cd1	slalyltransferase 8A (alpha-N-ac	622.4236	478	462.7941	520.9105	-4.28E-01	-3.82E-01	2	Unchanged Medium
Q9Y6A9	C05ef8	signal peptidase 12kDa	449.125	742	887.4615	692.8575	9.83E-01	7.24E-01	2	Unchanged Medium
P21378	I04ef3	signal peptidase complex (18kD)	630.5617	515	732.1592	626.0198	2.16E-01	-2.91E-01	2	Unchanged Medium
O15302	P10ab3	signal recognition particle 72kD	1040.23	818	841.5078	899.9534	-3.06E-01	-3.47E-01	2	Unchanged Medium
O76094	J02cd2	signal recognition particle 72kD	1473.56	965	1422.2	1286.822	-5.12E-02	-6.11E-01	2	Unchanged Medium
Q9UNL2	J10cd2	signal sequence receptor; gamm	1150.724	450	1654.744	1085.128	5.24E-01	-1.35E+00	2	Unchanged Medium
P40763	K09ef5	signal transducer and activator o	671.5038	545	348.0347	521.4351	-9.48E-01	-3.02E-01	2	Unchanged Medium
Q92783	M24cd3	signal transducing adaptor molec	827.9851	1020	725.7017	657.8322	-1.90E-01	3.01E-01	2	Unchanged Medium
Q9H723	N01gh5	similar to rat nuclear ubiquitous c	749.7661	530	1258.65	846.2392	7.47E-01	-5.06E-01	2	Unchanged Medium
O15258	A04cd7	similar to <i>S. cerevisiae</i> RER1	710.8499	635	933.6382	759.8427	3.93E-01	-1.63E-01	2	Unchanged Medium
O14834	A11cd7	similar to <i>S. pombe</i> dim1+	701.2292	753	903.8926	786.0877	3.66E-01	1.03E-01	2	Unchanged Medium
O43617	H05ef3	similar to yeast BET3 ( <i>S. cerevis</i>	1759.348	1750	1443.578	1650.871	-2.85E-01	-7.94E-03	2	Unchanged Medium
Q04837	G11cd2	single-stranded DNA binding pro	1264.277	894	1034.75	1064.292	-2.89E-01	-5.00E-01	2	Unchanged Medium
P05455	E19gh1	Sjogren syndrome antigen B (but	850.8691	744	930.6428	841.9268	1.29E-01	-1.93E-01	2	Unchanged Medium
P43331	K08cd2	small nuclear ribonucleoprotein t	918.3597	1260	1042.335	1073.82	1.86E-01	4.63E-01	2	Unchanged Medium
P09012	M12cd2	small nuclear ribonucleoprotein t	548.0261	310	685.6636	514.5708	3.23E-01	-8.22E-01	2	Unchanged Medium
P08579	A03cd2	small nuclear ribonucleoprotein t	502.6355	570	669.9879	581.0279	4.15E-01	1.83E-01	2	Unchanged Medium
P09234	A05cd2	small nuclear ribonucleoprotein t	1054.327	1450	1302.742	1269.64	3.05E-01	4.62E-01	2	Unchanged Medium
P08578	A07cd2	small nuclear ribonucleoprotein t	1901.214	1740	1818.557	1819.876	-6.41E-02	-1.28E-01	2	Unchanged Medium
Q15357	A11cd2	small nuclear ribonucleoprotein t	382.4892	734	593.847	570.2015	6.35E-01	9.41E-01	2	Unchanged Medium
P14678	C23cd3	small nuclear ribonucleoprotein t	2036.574	1280	1737.398	1686.178	-2.29E-01	-6.65E-01	2	Unchanged Medium
Q13487	P08cd1	small nuclear RNA activating cor	517.5819	684	648.0121	616.6789	3.24E-01	4.03E-01	2	Unchanged Medium
P35326	E17cd3	small proline-rich protein 2A	290.6174	1030	839.3072	721.2318	1.53E+00	1.93E+00	2	Unchanged Medium
P55854	H04cd2	SMT3 suppressor of mif two 3 ho	791.7437	658	962.4453	804.107	2.82E-01	-2.67E-01	2	Unchanged Medium
P14648	P19cd5	SNRNP ups/ear reading frame	1581.907	2270	1670.964	1839.36	7.90E-02	5.18E-01	2	Unchanged Medium
P55011	L17cd1	solute carrier family 12 (sodium/	591.8676	740	517.2382	618.497	-1.94E-01	3.23E-01	2	Unchanged Medium
O95258	P15cd4	solute carrier family 25 (mitochor	476.3075	518	577.8319	523.9535	2.79E-01	1.20E-01	2	Unchanged Medium
O15431	A21ab5	solute carrier family 31 (copper t	1227.872	1010	1769.026	1336.855	5.27E-01	-2.77E-01	2	Unchanged Medium
P04920	L04cd1	solute carrier family 4; anion excl	1614.362	1560	1704.134	1624.765	7.81E-02	-5.33E-02	2	Unchanged Medium
Q01650	J11ef5	solute carrier family 7 (callicrein	832.6996	632	1032.106	832.1088	3.10E-01	-3.99E-01	2	Unchanged Medium
Q07890	H23cd2	son of sevenless homolog 2 (Dro	476.9505	568	680.8529	575.1528	5.14E-01	2.51E-01	2	Unchanged Medium
O60749	A19cd2	sorting nexin 2	364.9343	931	769.5782	688.5915	1.06E+00	1.35E+00	2	Unchanged Medium
O60493	A09cd4	sorting nexin 3	1008.916	1350	1180.469	1180.399	2.27E-01	4.22E-01	2	Unchanged Medium
Q9Y5X3	G06ef4	sorting nexin 5	678.0975	647	688.5568	670.591	2.63E-02	-6.32E-02	2	Unchanged Medium
Q01082	E09cd2	spectrin; beta; non-erythrocytic 1	571.4909	679	387.0403	545.8922	-5.62E-01	2.49E-01	2	Unchanged Medium
P52788	M10cd2	sperrmine synthase	695.1994	854	770.002	639.7693	-2.17E-01	-6.78E-02	2	Unchanged Medium
P17947	C19cd2	spleen focus forming virus (SFFV	1307.418	1150	1646.278	1366.573	3.32E-01	-1.90E-01	2	Unchanged Medium
Q14818	D10ef6	splicing factor 1	547.0998	499	782.2929	609.3562	5.16E-01	-1.34E-01	2	Unchanged Medium
Q15427	K11cd6	splicing factor 3b; subunit 4; 49kd	441.2394	612	540.0723	530.9445	2.92E-01	4.71E-01	2	Unchanged Medium
Q15815	M06cd2	splicing factor; arginine/serine-ri	739.2591	553	551.9082	614.261	-4.20E-01	-4.18E-01	2	Unchanged Medium
Q01130	H22cd1	splicing factor; arginine/serine-ri	553.5808	527	488.5465	522.9409	-1.80E-01	-7.18E-02	2	Unchanged Medium
P23152	H24cd1	splicing factor; arginine/serine-ri	1547.474	1460	1428.273	1480.13	-1.16E-01	-7.94E-02	2	Unchanged Medium
Q13503	L22cd4	SRB7 suppressor of RNA polyme	712.8859	574	725.0591	670.5377	2.44E-02	-3.13E-01	2	Unchanged Medium
Q9P2R9	C23ef2	SRP25 nuclear protein	495.796	558	515.095	522.8318	5.51E-02	1.69E-01	2	Unchanged Medium
Q9H612	F07gh5	SRY (sex determining region Y)4	774.5162	970	714.8668	819.674	-1.16E-01	3.24E-01	2	Unchanged Medium
Q9BT81	I13gh8	SRY (sex determining region Y)4	497.0608	530	550.1706	525.7297	1.46E-01	9.25E-02	2	Unchanged Medium

O60526	M03cd6	STIP1 homology and U-Box cont	706.6078	538	543.7559	596.1019	-3.78E-01	-3.93E-01	2	Unchanged Medium
Q9Y6X1	A21e4	stress-associated endoplasmic r	1683.36	1220	2201.847	1700.638	3.87E-01	-4.68E-01	2	Unchanged Medium
P31948	M15ef3	stress-induced-phosphoprotein 1	436.1143	549	517.5934	500.9139	2.47E-01	3.32E-01	2	Unchanged Medium
P21912	E09gh1	succinate dehydrogenase compl	701.7228	902	751.7357	785.3111	9.93E-02	3.63E-01	2	Unchanged Medium
O14521	H04cd1	succinate dehydrogenase compl	628.8405	505	672.375	601.9355	9.66E-02	-3.18E-01	2	Unchanged Medium
P53597	I09gh1	succinate-CoA ligase; GDP-formi	704.4006	491	553.293	582.7447	-3.48E-01	-5.22E-01	2	Unchanged Medium
O95605	P15cd5	SUMO-1 activating enzyme subu	776.4199	499	433.2742	569.4163	-8.42E-01	-6.39E-01	2	Unchanged Medium
Q16550	K01cd2	suppressor of Ty 4 homolog 1 (S	813.5735	1440	991.3588	1081.744	2.85E-01	8.24E-01	2	Unchanged Medium
Q15526	K07cd2	surfeit 1	468.3614	522	583.8097	524.7026	3.18E-01	1.56E-01	2	Unchanged Medium
O43539	P02cd1	SWI/SNF related; matrix associ	1047.14	1280	1212.614	1178.519	2.12E-01	2.85E-01	2	Unchanged Medium
Q9UPX1	D23cd7	synaptopodin	683.4973	536	421.1841	548.8885	-6.98E-01	-3.51E-01	2	Unchanged Medium
O95721	O09cd5	synatosomal-associated protein	830.7721	1030	686.6755	849.1506	-2.75E-01	3.10E-01	2	Unchanged Medium
O43391	H09cd2	syndecan binding protein (synter	825.8962	640	379.1899	548.1569	-7.23E-01	3.17E-02	2	Unchanged Medium
Q15833	J04cd2	syntaxin binding protein 2	661.0175	556	840.6951	686.0183	3.47E-01	-2.49E-01	2	Unchanged Medium
Q92804	T20cd3	TAF15 RNA polymerase II; TATA	673.5584	605	1063.778	847.4936	2.84E-01	-5.30E-01	2	Unchanged Medium
Q9Y490	B04cd2	talin 1	1342.238	1170	2365.625	1625.187	8.18E-01	-2.01E-01	2	Unchanged Medium
O94797	H20e7	Tara-like protein	899.0807	448	496.1404	614.3777	-8.58E-01	-1.01E+00	2	Unchanged Medium
Q13311	C05cd6	Tax1 (human T-cell leukemia vir	899.9979	1190	926.2314	1004.505	4.15E-02	4.00E-01	2	Unchanged Medium
Q16650	F08cd6	T-box; brain; 1	1407.309	1750	1777.889	1645.184	3.37E-01	3.15E-01	2	Unchanged Medium
P51864	P04ef7	teratocarcinoma-derived growth i	2037.212	1590	1447.46	1690.282	-4.93E-01	-3.61E-01	2	Unchanged Medium
P55061	O19cd2	testis enhanced gene transcript	1540.968	1330	1972.323	1615.143	3.56E-01	-2.10E-01	2	Unchanged Medium
Q15569	P21cd2	testis-specific kinase 1	837.6269	796	708.1178	780.661	-2.42E-01	-7.31E-02	2	Unchanged Medium
O60636	F08cd5	tetraspan 2	468.1664	702	375.3225	515.2157	-3.19E-01	5.85E-01	2	Unchanged Medium
O60637	F06cd5	tetraspan 3	1025.362	742	545.9662	770.9441	-9.09E-01	-4.68E-01	2	Unchanged Medium
O95857	F13ef3	tetraspan NET-6 protein	702.1579	676	359.1921	578.9636	-9.67E-01	-5.58E-02	2	Unchanged Medium
Q99614	M03cd3	tetrastricopeptide repeat domain 1	706.3536	891	635.5379	744.2616	-1.52E-01	3.35E-01	2	Unchanged Medium
Q13118	L05cd2	TGFB Inducible early growth res	445.9691	601	679.2931	575.4732	6.07E-01	4.31E-01	2	Unchanged Medium
Q15563	A16cd2	TGF $\beta$ -Induced factor (TALE fam)	885.9	1290	1140.439	1105.268	3.64E-01	5.42E-01	2	Unchanged Medium
Q9H3N1	N03gh7	thioredoxin domain-containing	409.6333	426	686.7997	507.428	7.46E-01	5.60E-02	2	Unchanged Medium
O43396	O17cd5	thioredoxin-like; 32kD	1821.595	1710	1548.596	1693.179	-2.34E-01	-9.18E-02	2	Unchanged Medium
P04216	B02cd2	Thy-1 cell surface antigen	169.8064	298	4157.367	1541.609	4.61E+00	8.10E-01	2	Unchanged Medium
P12956	K10ef5	thyroid autoantigen 70kD (Ku anl	1172.56	1490	1395.803	1353.001	2.51E-01	3.46E-01	2	Unchanged Medium
P16035	P11ef7	tissue inhibitor of metalloproteinase	360.2533	354	913.1351	542.4517	1.34E+00	-2.54E-02	2	Unchanged Medium
Q9H2X8	J08gh8	TL2H9 protein precursor	710.2447	1000	1386.102	1033.648	9.65E-01	5.00E-01	2	Unchanged Medium
Q13077	L11cd2	TNF receptor-associated factor 1	1265.054	1270	756.401	1097.404	-7.42E-01	6.49E-03	2	Unchanged Medium
Q9NZ34	P08gh4	TPA regulated locus	1074.319	1090	1284.44	1148.575	2.58E-01	1.69E-02	2	Unchanged Medium
Q15369	D18ef5	transcription elongation factor B-	771.5598	1100	693.1767	854.8396	-1.55E-01	5.11E-01	2	Unchanged Medium
Q15906	P11ef6	transcription factor-like 1	436.5561	510	878.9083	508.5936	1.01E+00	2.25E-01	2	Unchanged Medium
P50816	H08cd5	transducer of ERBB2; 1	888.8059	874	518.1816	760.3803	-7.78E-01	-2.40E-02	2	Unchanged Medium
Q13595	N04ef7	transformer-2 alpha (htra-2 alpha)	247.4437	612	698.379	519.219	1.50E+00	1.31E+00	2	Unchanged Medium
P37802	F05cd3	transitional epithelia response pr	1324.284	2240	1173.434	1796.473	1.70E-01	1.70E-01	2	Unchanged Medium
Q9Y5Z9	D01cd8	translocase of inner mitochondria	1986.716	875	1126.793	1108.824	-2.33E-01	-5.97E-01	2	Unchanged Medium
Q99595	K10cd6	translocase of inner mitochondria	450.6578	665	448.5161	521.2602	-6.87E-03	5.60E-01	2	Unchanged Medium
O50830	A09cd6	translocase of inner mitochondria	1646.564	1590	1992.925	1744.175	2.75E-01	-4.77E-02	2	Unchanged Medium
O14925	I24cd6	translocase of inner mitochondria	745.8102	813	633.4301	737.451	-1.91E-01	1.25E-01	2	Unchanged Medium
Q9Y5J9	E08cd8	translocase of inner mitochondria	1641.377	1550	1653.524	1615.991	1.06E-02	-7.98E-02	2	Unchanged Medium
Q15629	G18ef3	translocating chain-associating n	1003.031	1060	624.4499	897.0752	-6.84E-01	8.48E-02	2	Unchanged Medium
Q99442	C10cd2	translocation protein 1	526.8783	772	1065.397	788.001	1.02E+00	5.51E-01	2	Unchanged Medium
Q99805	A18cd5	transmembrane 9 superfamily me	1023.368	1260	957.2801	1081.028	-9.63E-02	3.03E-01	2	Unchanged Medium
Q9V2B0	C20ef3	transmembrane protein 4	681.3857	1320	985.8397	995.6424	5.33E-01	9.54E-01	2	Unchanged Medium
P49755	J05ef4	transmembrane trafficking protei	1311.203	459	700.7243	827.066	-9.04E-01	-1.48E+00	2	Unchanged Medium
F03gh4		transmembrane; prostate androg	1287.98	841	662.4165	930.4505	-9.59E-01	-6.15E-01	2	Unchanged Medium
Q03519	B07cd1	transporter 2; ATP-binding casse	851.2148	573	580.8519	701.534	-3.22E-01	-5.72E-01	2	Unchanged Medium
Q9NWF9	P02gh2	TRIAD3 protein	665.9772	444	688.6646	599.4053	4.83E-02	-5.86E-01	2	Unchanged Medium
Q15656	O07ef7	TRK-fused gene	1878.254	1640	1858.307	1792.501	-1.54E-02	-1.95E-01	2	Unchanged Medium
Q92734	J17cd7	TRK-fused gene	1450.307	1810	1609.067	1624.429	1.50E-01	3.23E-01	2	Unchanged Medium
Q12815	A21ef7	triphthine associated protein (last	821.5601	1100	722.8544	879.798	-1.85E-01	4.15E-01	2	Unchanged Medium
P09493	O02cd1	trypomysin 1 (alpha)	988.1694	429	1004.982	807.373	2.43E-02	-1.20E+00	2	Unchanged Medium
P49411	M11cd3	Tu translation elongation factor	525.8572	555	476.4592	519.255	-1.42E-01	7.90E-02	2	Unchanged Medium
P05217	F03gh6	tubulin; beta; 2	1203.686	705	920.1831	942.8088	-3.87E-01	-7.73E-01	2	Unchanged Medium
P23258	K03cd3	tubulin; gamma 1	1733.971	1220	2149.365	1702.331	3.10E-01	-5.03E-01	2	Unchanged Medium
Q9UBN6	A16ef5	tumor necrosis factor receptor su	470.7412	751	531.524	584.4772	1.75E-01	6.74E-01	2	Unchanged Medium
Q13292	L22ef4	tumor necrosis factor; alpha-indu	849.276	792	552.7776	731.2933	-6.20E-01	-1.01E-01	2	Unchanged Medium
O00496	K21cd3	tumor suppressing subtransferab	628.3509	554	800.8751	661.0848	3.50E-01	-1.82E-01	2	Unchanged Medium
Q99816	G04cd4	tumor susceptibility gene 101	723.8133	766	627.1295	705.4904	-2.07E-01	8.08E-02	2	Unchanged Medium
P16422	K03ab7	tumor-associated calcium signal	1448.512	791	373.663	670.9367	-1.95E+00	-8.73E-01	2	Unchanged Medium
Q9NP84	K03ef2	type I transmembrane protein Fn	691.89	498	560.2824	583.2792	-3.04E-01	-4.75E-01	2	Unchanged Medium
Q9UJ47	O09cd8	type I transmembrane receptor (s	792.9873	819	809.9056	807.3703	3.05E-02	4.69E-02	2	Unchanged Medium
P31946	K21ef6	tyrosine 3-monooxygenase/trypt	1220.9989	955	724.9989	966.9847	-7.52E-01	-3.55E-01	2	Unchanged Medium
P35214	J19ef4	tyrosine 3-monooxygenase/trypt	881.0131	989	682.5327	850.9964	-3.68E-01	1.67E-01	2	Unchanged Medium
P27348	G15cd7	tyrosine 3-monooxygenase/trypt	2196.334	1540	1104.855	1615.078	-9.91E-01	-5.08E-01	2	Unchanged Medium
O60704	J01cd3	tyrosylprotein sulfotransferase 2	658.3761	299	686.1339	547.7036	5.96E-02	-1.14E+00	2	Unchanged Medium
Q9Y4Z0	G09cd8	U1 snRNA-associated Sm-like pr	837.5087	689	914.9547	813.8478	1.28E-01	-2.81E-01	2	Unchanged Medium
P14927	G05cd4	ubiquinol-cytochrome c reductas	995.1237	817	954.3085	922.1475	-6.04E-02	-2.85E-01	2	Unchanged Medium
Q9UJ02	P18ef7	ubiquinol-cytochrome c reductas	953.6884	1460	1546.568	1320.75	6.97E-01	6.16E-01	2	Unchanged Medium
P31930	A22cd3	ubiquinol-cytochrome c reductas	846.6396	849	686.9864	794.0747	-3.01E-01	3.33E-03	2	Unchanged Medium
P22695	A24cd3	ubiquinol-cytochrome c reductas	468.5936	636	581.791	562.0633	3.12E-01	4.40E-01	2	Unchanged Medium
P07919	E08cd4	ubiquinol-cytochrome c reductas	1328.532	1810	1005.378	1382.391	-4.02E-01	4.49E-01	2	Unchanged Medium
P47985	E06cd4	ubiquinol-cytochrome c reductas	1519.763	1270	1127.575	1306.086	-4.31E-01	-2.58E-01	2	Unchanged Medium
Q9NZ09	N17ef1	ubiquitin associated protein	1588.177	1820	1392.592	1598.619	-1.90E-01	1.93E-01	2	Unchanged Medium
Q9UNP0	F09gh6	ubiquitin specific protease 15	525.3364	492	597.7817	538.3523	1.86E-01	-9.48E-02	2	Unchanged Medium
Q9UHP3	L21cd1	ubiquitin specific protease 25	554.0657	724	561.5817	613.0845	1.94E-02	3.85E-01	2	Unchanged Medium
P22314	O07cd3	ubiquitin-activating enzyme E1 (	1857.238	1640	1663.316	1788.503	4.71E-03	-1.75E-01	2	Unchanged Medium
Q13404	O23cd3	ubiquitin-conjugating enzyme E2	1073.414	1210	1128.562	1138.559	7.28E-02	1.77E-01	2	Unchanged Medium
P51659	D05cd4	ubiquitin-conjugating enzyme E2	1266.25	1300	1173.73	1247.427	-1.09E-01	4.05E-02	2	Unchanged Medium
P47986	O11cd3	ubiquitin-conjugating enzyme E2	616.3689	520	567.7317	567.8765	-1.19E-01	-2.47E-01	2	Unchanged Medium

Q14933	H14cd4	ubiquitin-conjugating enzyme E2	717.4244	893	596.8415	735.6835	-2.66E-01	3.16E-01	2	Unchanged	Medium
Q16781	D07cd4	ubiquitin-conjugating enzyme E2	923.6537	816	533.7389	757.964	-7.91E-01	-1.78E-01	2	Unchanged	Medium
Q93068	A02cd3	ubiquitin-like 1 (sentrin)	1376.087	1530	1294.307	1399.48	-8.84E-02	1.51E-01	2	Unchanged	Medium
Q15386	H10gh1	ubiquitin-protein isopeptidase ligase	531.8659	630	628.2454	596.6866	2.40E-01	2.45E-01	2	Unchanged	Medium
QSUBK9	I15cd4	ubiquitously-expressed transcript	936.2619	1080	1384.764	1125.743	5.65E-01	1.74E-01	2	Unchanged	Medium
O60512	E11ab3	UDP-Gal-betaGlcNAc beta 1,4- <i>s</i>	436.7634	610	542.39	529.5839	3.12E-01	4.81E-01	2	Unchanged	Medium
P78383	P20cd5	UDP-galactose transporter relate	1570.135	1700	2180.117	1816.963	4.74E-01	1.15E-01	2	Unchanged	Medium
Q16851	I24cd4	UDP-glucose pyrophosphorylase	1324.08	1260	1318.78	1302.468	-5.79E-03	-6.64E-02	2	Unchanged	Medium
Q9NZ45	L02gh3	uncharacterized hematopoietic si	652.0685	670	696.5692	672.8895	9.52E-02	3.98E-02	2	Unchanged	Medium
Q9NZ32	L20gh4	uncharacterized hypothalamus p	1035.575	1250	1354.231	1214.412	3.87E-01	2.75E-01	2	Unchanged	Medium
Q9NZ29	L15gh4	uncharacterized hypothalamus p	659.53	992	1118.776	923.518	7.62E-01	5.89E-01	2	Unchanged	Medium
Q15853	C02cd3	upstream transcription factor 2; c	601.6839	635	698.0128	644.9023	2.14E-01	7.78E-02	2	Unchanged	Medium
Q92528	D02ef7	uridine monophosphate kinase	560.3976	685	623.5243	623.0076	1.54E-01	2.90E-01	2	Unchanged	Medium
P15692	M04ef7	vascular endothelial growth facto	460.9257	539	857.3953	619.202	8.95E-01	2.27E-01	2	Unchanged	Medium
P50552	C08cd3	vasodilator-stimulated phosphop	468.4573	648	392.5569	502.9122	-2.55E-01	4.67E-01	2	Unchanged	Medium
O60763	H16cd3	vesicle docking protein p115	639.538	543	745.4806	642.7624	2.21E-01	-2.35E-01	2	Unchanged	Medium
Q15836	A15ef5	vesicle-associated membrane pn	804.2648	1370	1060.211	1076.578	3.99E-01	7.63E-01	2	Unchanged	Medium
Q8UEU0	O22cd6	vesicle-associated soluble NSF t	468.6024	697	698.3534	621.1953	5.76E-01	5.72E-01	2	Unchanged	Medium
P14921	E24ef5	v-ets erythroblastosis virus E26 t	913.893	765	291.1538	656.6528	-1.65E+00	-2.57E-01	2	Unchanged	Medium
P18206	C14cd3	vinculin	580.3315	857	865.7505	767.5496	5.77E-01	5.62E-01	2	Unchanged	Medium
P00540	G08ef5	v-mos Moloney murine sarcoma	1115.145	728	663.6747	835.5051	-7.49E-01	-6.16E-01	2	Unchanged	Medium
P01106	E18ef5	v-myc myelocytomatosis viral on	537.8131	601	405.1047	514.7639	-4.09E-01	1.61E-01	2	Unchanged	Medium
P21796	C16cd3	voltage-dependent anion channe	483.8969	510	584.201	525.9036	2.72E-01	7.47E-02	2	Unchanged	Medium
Q15765	C12cd3	von Hippel-Lindau binding protel	689.743	705	891.2621	762.0788	3.70E-01	3.20E-02	2	Unchanged	Medium
P10398	D01ab4	v-raf murine sarcoma 3611 viral t	1061.812	639	532.2153	744.4583	-9.96E-01	-7.32E-01	2	Unchanged	Medium
P12233	A19ef6	v-ral simian leukemia viral oncog	848.7099	1060	1081.428	995.8044	3.50E-01	3.17E-01	2	Unchanged	Medium
Q9Y6W5	A22gh1	WAS protein family; member 2	1283.077	1630	1493.145	1468.514	2.19E-01	3.45E-01	2	Unchanged	Medium
Q9UPY6	L06cd6	WAS protein family; member 3	1503.584	1210	2151.643	1623.108	5.17E-01	-3.09E-01	2	Unchanged	Medium
O75083	D15cd5	WD repeat domain 1	892.4425	977	963.3448	944.1492	1.10E-01	1.30E-01	2	Unchanged	Medium
O76071	A24cd5	WD40 protein Cdc41	609.8821	898	730.5311	746.1814	2.60E-01	5.58E-01	2	Unchanged	Medium
Q9HCN4	H11gh6	XPA binding protein 1; putative A	1199.21	1070	507.3277	923.9753	-1.24E+00	-1.71E-01	2	Unchanged	Medium
Q9UJW05	N17ef3	yeast Sec31p homolog	1887.447	1590	1542.778	1672.59	-2.91E-01	-2.50E-01	2	Unchanged	Medium
Q9UQR1	P06gh1	zinc finger protein 148 (pHZ-52)	513.8639	737	563.7625	604.9201	1.34E-01	5.21E-01	2	Unchanged	Medium
Q14119	G21ef5	zinc finger protein 161	1199.558	1760	1197.34	1387.253	-2.67E-03	5.57E-01	2	Unchanged	Medium
Q9NW07	F06gh2	zinc finger protein 358	402.8342	575	684.7069	554.3431	7.65E-01	5.15E-01	2	Unchanged	Medium
P20694	D04ef6	zinc finger protein 9 (a cellular re	1042.65	1010	856.5924	969.9823	-2.84E-01	-4.49E-02	2	Unchanged	Medium

**WHAT IS CLAIMED IS:**

1. A method for expanding mammalian acinar cells, comprising culturing said cells in a cell culture system comprising a cell culture medium and a cell attachment surface, under conditions wherein said acinar cells undergo a 3-4 fold expansion together with transdifferentiation into a modified cell phenotype (IP cells) showing characteristics of acinar cells and liver cells.
2. The method of claim 1, wherein said cells having a modified phenotype express cytokeratin 18 (CK18), CK8, CK19, CK7, HNF1, alpha-1 antitrypsin, pi-glutathione s transferase (pi-GST), liver-specific bHLH transcription factor, Thy-1, C/EBP-alpha and C/EBP-beta, and express little if any carbonic anhydrase, cystic fibrosis transmembrane conductance regulator (CFTR), elastase and amylase.
3. The method of claim 1, wherein said culture medium comprises insulin, transferrin, selenium and epidermal growth factor (EGF) in a base medium suitable for maintaining epithelial cells.
4. The method of claim 1, wherein said culture medium comprises serum.
5. The method of claim 4, wherein said culture medium comprises up to 15% serum.
6. The method of claim 1, wherein said culture medium is serum-free.
7. The method of claim 1, wherein said cell culture medium comprises an effective amount of at least one soluble active factor that promotes growth expansion and transdifferentiation of acinar cells to IP cells.
8. The method of claim 7, wherein said culture medium comprises an effective amount of at least one factor selected from the group consisting of heat inactivated bovine serum albumin (BSA) and the soluble active factors hepatocyte growth factor (HGF), insulin-like growth factor-1 (IGF-1), transforming growth factor alpha (TGF- $\alpha$ ), betacellulin, gastrin I and prolactin.
9. The method of claim 7, wherein said culture medium comprises an effective amount of at least one soluble active factor selected from the group consisting of HGF, betacellulin and prolactin.
10. The method of claim 1, wherein said cell attachment surface comprises one or more extracellular matrix molecules.

11. The method of claim 10, wherein said cell attachment surface comprises one or more extracellular matrix molecules selected from the group consisting of Collagen I, Collagen VI, Collagen IV, Vitronectin and Fibronectin.
12. The method of claim 1, wherein the cells are seeded at a density of  $10^3 - 10^5$  cells/cm<sup>2</sup>.
13. The method of claim 1, wherein the cells are cultured for a period of 4-8 days.
14. The method of claim 1, wherein the acinar cells are human acinar cells.
15. The method of claim 1 wherein the acinar cells undergo transdifferentiation from an amylase+ acinar phenotype to an amylase+/CK19+ mixed acinar/liver-specific phenotype.
16. A culture medium comprising a base medium suitable for maintaining mammalian epithelial cells that includes insulin, transferrin, selenium and EGF, wherein cultivation of human acinar cells in said medium under suitable conditions for 4-8 days results in expansion of said cells by 3-4 fold and transdifferentiation into a modified cell phenotype showing characteristics of acinar and liver cells.
17. The culture medium of claim 16, wherein the base medium comprises DMEM, Hams F12, MEM, M-199, or RPMI, or a combination thereof.
18. The culture medium of claim 17, wherein the base medium comprises 4 mM glutamine and a 1:1 mixture of DMEM and Hams 12.
19. The culture medium of claim 16, which additionally comprises serum.
20. The culture medium of claim 19, which additionally comprises up to 15% serum.
21. The culture medium of claim 16, which is serum-free.
22. The cell culture medium of claim 16, which comprises about 0.1-10 µg/ml insulin, about 0.5-10 µg/ml transferrin, about 0.25 - 5.0 ng/ml selenium, and about 1-20 ng/l EGF.
23. The cell culture medium of claim 16, which additionally comprises an effective amount of at least one soluble active factor that promotes expansion and transdifferentiation of acinar cells into IP cells.
24. The cell culture medium of claim 16, which additionally comprises an effective amount of at least one factor selected from the group consisting of heat-

- inactivated BSA and the soluble active factors albumin, HGF, IGF-1, TGF- $\alpha$ , betacellulin, gastrin I and prolactin.
- 25. The cell culture medium of claim 24, wherein the concentration of BSA is 0.1-2%, the concentration of HGF is 1-20 ng/ml, the concentration of IGF-1 is 0.5-50 ng/ml, the concentration of TGF- $\alpha$  is 1-10 ng/ml, the concentration of betacellulin is 0.0005-0.1 ug/ml, the concentration of gastrin I is 1-100 pg/ml, and the concentration of prolactin is 1-10 ng/ml.
  - 26. The cell culture medium of claim 24, which comprises an effective amount of at least one soluble active factor selected from the group consisting of HGF, betacellulin and prolactin.
  - 27. A cell culture system, which comprises the cell culture medium of claim 16 and a cell attachment surface.
  - 28. The cell culture system of claim 27, wherein the cell attachment surface comprises a composition selected from the group consisting of collagen I, collagen VI, collagen IV, vitronectin and fibronectin.
  - 29. An isolated mammalian cell having a phenotype comprising both acinar and liver-associated markers.
  - 30. The isolated cell of claim 29 that expresses least one marker selected from the group consisting of CK18, CK8, CK19, CK7, HNF1, alpha-1 antitrypsin, pi-glutathione s transferase (pi-GST), liver-specific bHLH transcription factor, Thy-1, C/EBP-alpha and C/EBP-beta; and that expresses little or none of the following markers: carbonic anhydrase, cystic fibrosis transmembrane conductance regulator (CFTR), elastase and amylase.
  - 31. The isolated cell of claim 29 that expresses CK18, CK8, CK19, CK7, HNF1, alpha-1 antitrypsin, pi-glutathione s transferase (pi-GST), liver-specific bHLH transcription factor, Thy-1, C/EBP-alpha and C/EBP-beta.
  - 32. The isolated cell of claim 29 that is derived from a primary culture of pancreatic acinar cells.
  - 33. The isolated cell of claim 29 that is human.
  - 34. The isolated cell of claim 29 having an expression profile after 8 days *ex vivo* as shown in Table 6.

35. An isolated cell prepared by the method of claim 1.
36. A kit suitable for expanding mammalian acinar cells, comprising
  - a) a base medium suitable for the cultivation of mammalian epithelial cells,
  - b) a collagen I coated culture substrate, and, separately packaged,
  - c) a serum-free medium supplement containing one or more component selected from the group consisting of BSA, HGF, EGF, TGFA, betacellulin, gastrin I and IGF-1.
37. The kit of claim 36, wherein the serum-free medium supplement contains components in as suitable ratio for producing a medium containing 0.1-2% BSA, 1-20 ng/ml HGF, 1-20 ng/ml EGF, 1-10 ng/ml TGFA, 0.0005-0.10 ug/ml betacellulin, 1.0-100 pg/mL gastrin1, and 0.5-50 ng/mL IGF1, by the addition of a predetermined amount of base medium.
38. The kit of claim 36 wherein the cell culture substrate is on the surface of a flask, bottle, petri dish, plate or well, or is part of a scaffold, suitable for cell culture.
39. A method for transforming IP cells that express markers of acinar cells and liver-associated genes into insulin-producing cells *in vitro*, comprising culturing said IP cells in a cell culture medium comprising an effective amount of at least one differentiation promoting factor selected from the group consisting of Activin A, acidic FGF, basic FGF, C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit, Dexamethasone, Gastrin-Releasing Peptide, Glucagon-like Peptide-1 (GLP-1), Glucose, IGF1, IGF2, Insulin, Laminin, LIF, Met-Enkephalin, PDGFAA+PDGFBB, Prolactin, Sonic Hedgehog, Substance P, TGF-alpha, Trolox (alpha-tocopherol derivative), and VEGF, such that the IP cells are transformed into insulin-producing cells.
40. The method of claim 39, wherein the IP cells are derived from a culture of pancreatic acinar cells.
41. The method of claim 40, wherein the cells are human.
42. The method of claim 39, further comprising contacting said cells with a substrate that is coated with one or more extracellular matrix molecules.
43. The method of claim 42, wherein the extracellular matrix molecules are collagen I, collagen VI, collagen IV, vitronectin, and/or fibronectin.

44. The method of claim 42, wherein the substrate is on the surface of a flask, petri dish, plate, well or roller bottle, or is part of a scaffold.
45. The method of claim 39, wherein the medium is serum-free.
46. The method of claim 39, wherein the medium comprises serum.
47. The method of claim 46, wherein the medium comprises BSA, insulin, transferrin, selenium and epidermal growth factor (EGF).
48. The method of claim 39, wherein the cells are seeded on the substrate at a density of  $5 \times 10^3$  to  $20 \times 10^5$  cells/cm<sup>2</sup>.
49. An isolated insulin-producing cell generated by the method of claim 39.
50. An insulin-producing cell, prepared by differentiating a mammalian acinar cell *in vitro*, wherein said insulin-producing cell has an expression profile after 16 days *ex vivo* as shown in Table 6.
51. A serum-free medium comprising at least one active factor selected from the group consisting of Activin A, acidic FGF, basic FGF, C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit, Dexamethasone, Gastrin-Releasing Peptide, Glucagon-like Peptide-1 (GLP-1), Glucose, IGF1, IGF2, Insulin, Laminin, LIF, Met-Enkephalin, PDGFAA+PDGFBB, Prolactin, Sonic Hedgehog, Substance P, TGF-alpha, Trolox (alpha-tocopherol derivative), and VEGF, wherein said medium facilitates differentiation of IP cells into insulin-producing cells.
52. A serum-free medium comprising a 1:1 mixture of DMEM and Hams F12 plus the components listed in Table 2.
53. A kit suitable for differentiating IP cells to insulin-producing cells, comprising
  - a) a base medium suitable for the cultivation of mammalian epithelial cells;
  - b) a collagen I coated culture substrate, and, separately packaged,
  - c) a serum-free medium supplement containing BSA, Activin A, acidic FGF, basic FGF, C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit, Dexamethasone, Gastrin-Releasing Peptide, Glucagon-like Peptide-1 (GLP-1), Glucose, IGF1, IGF2, Insulin, Laminin, LIF, Met-Enkephalin, PDGFAA+PDGFBB, Prolactin, Sonic Hedgehog, Substance P, TGF-alpha, Trolox (alpha-tocopherol derivative), or VEGF, or two or more of these

components in combination, in suitable amounts to yield final concentrations in the completed medium as indicated in Table 1 herein.

54. The kit of claim 53, wherein the cell culture substrate is contained on the surface of a flask, bottle, petri dish, plate or well suitable for cell culture.
55. A method for obtaining insulin-producing cells through culture and manipulation of pancreatic acinar cells *in vitro* comprising the steps of
  - i) culturing pancreatic acinar cells in a cell culture system comprising a culture medium and a cell attachment surface, under conditions wherein said acinar cells undergo a 3-4 fold expansion together with transdifferentiation into partially differentiated IP cells that express cytokeratin 18 (CK18), CK8, CK19, CK7, HNF1, alpha-1 antitrypsin, pi-glutathione s transferase (pi-GST), liver-specific bHLH transcription factor, Thy-1, C/EBP-alpha and C/EBP-beta; and that express little if any of carbonic anhydrase, cystic fibrosis transmembrane conductance regulator (CFTR), elastase and amylase; and
  - ii) culturing said IP cells in a cell culture system comprising a cell culture medium and a substrate, said culture medium comprising an effective amount of at least one differentiation promoting factor selected from the group consisting of Activin A, acidic FGF, basic FGF, C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit, Dexamethasone, Gastrin-Releasing Peptide, Glucagon-like Peptide-1 (GLP-1), Glucose, IGF1, IGF2, Insulin, Laminin, LIF, Met-Enkephalin, PDGFAA+PDGFBB, Prolactin, Sonic Hedgehog, Substance P, TGF-alpha, Trolox (alpha-tocopherol derivative), and VEGF; such that the IP cells are transformed into insulin-producing cells.
56. The method of claim 55, wherein said insulin-producing cells release c-peptide and/or insulin in response to exposure to glucose.
57. The method of claim 55, wherein the medium of step i) comprises an HGF receptor activator and an EGF receptor activator.
58. The method of claim 55, wherein the medium of step ii) comprises an effective amount of at least one soluble active factor selected from the group consisting of C-Natriuretic Peptide (CNP), Calcitonin Gene Related Peptide, Cholera Toxin B Subunit,

- Dexamethasone, Gastrin-Releasing Peptide, Laminin, Met-Enkephalin, PDGFAA+PDGFBB, Sonic Hedgehog, and Substance P.
59. A method of obtaining insulin-producing cells, said method comprising culturing primary pancreatic cells in a two phase culture system whereby, in the first phase, the cells are cultured on a surface comprising an effective amount of at least one ECM in a medium comprising at least one active soluble factor selected from the group consisting of HGF, TGF $\alpha$ , EGF, IGF1, betacellulin, prolactin and gastrin 1 for 4-10 days; and in a second phase, the cells are cultured on a surface comprising at least one ECM in a medium comprising an effective amount of at least one differentiation promoting factor selected from the group consisting of Activin A, CGRP alpha, C natiriuretic peptide (CNP), Cholera Toxin B Subunit, Dexamethasone, aFGF, Glucagon-Like Peptide-1 (GLP-1), Glucose, Insulin, LIF, PDGFAA, PDGFBB, TGF-alpha, Prolactin, Trolox (Vitamin E), Gastrin Releasing Peptide (GRP), IGF-1, IGF-2, Laminin, Met-Enkephalin, Sonic hedgehog, Substance P, bFGF, and VEGF for 3-14 days to obtain insulin producing cells.
60. A primary culture of insulin-producing cells derived from glandular epithelial cells that expressed at least one marker selected from the group consisting of : cytokeratin 18 (CK18), CK8, CK19, CK7, HNF1, alpha-1 antitrypsin, pi-glutathione s transferase (pi-GST), liver-specific bHLH transcription factor, Thy-1, C/EBP-alpha and C/EBP-beta; and that expressed little if any of the markers carbonic anhydrase, cystic fibrosis transmembrane conductance regulator (CFTR), elastase and amylase, said insulin-producing cells having the characteristics of forming three-dimensional cell clusters that contain proinsulin and/or insulin and/or c-peptide.
61. The culture of claim 60 wherein the glandular epithelial cells are pancreatic cells.
62. The culture of claim 60 wherein the culture releases insulin and/or c-peptide in response to a glucose challenge.
63. The culture of claim 60, wherein the glandular epithelial cells are human.



FIG. 1A

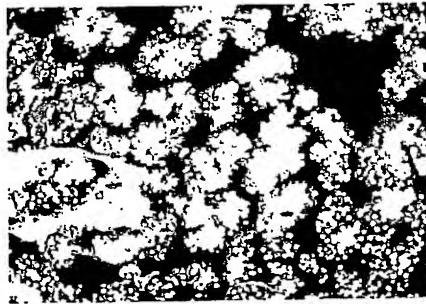


FIG. 1C

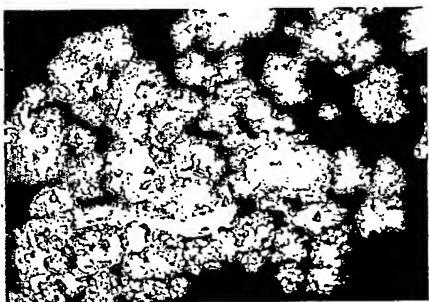


FIG. 1B

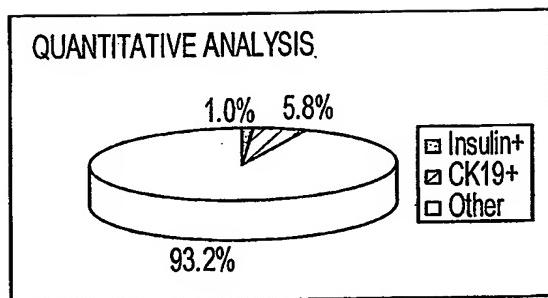


FIG. 1D

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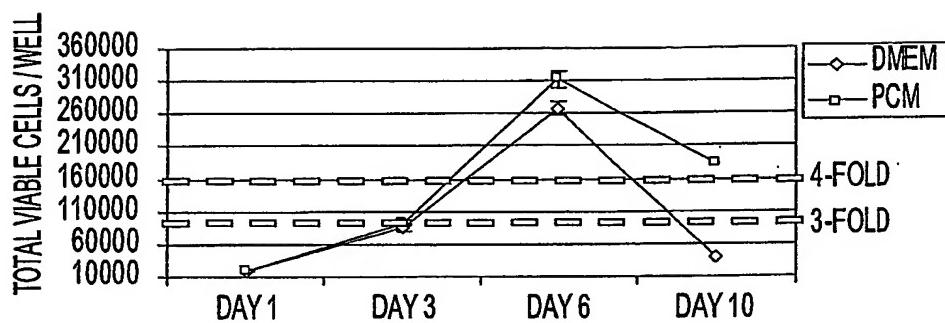


FIG. 2A

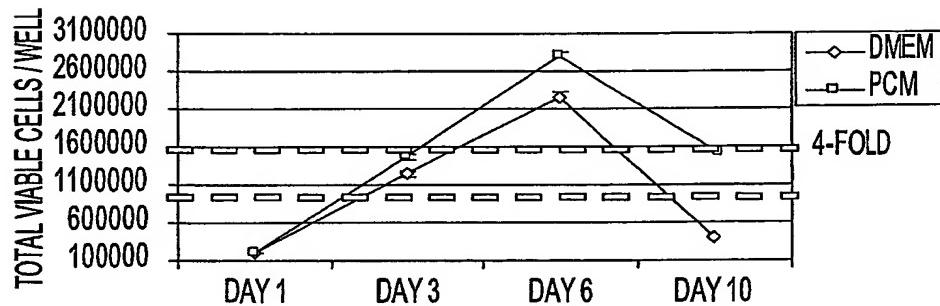


FIG. 2B

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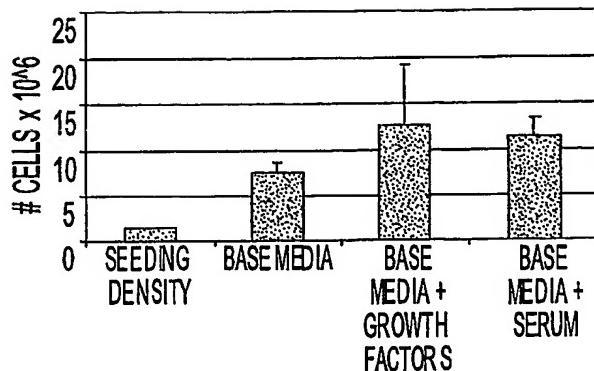


FIG. 3

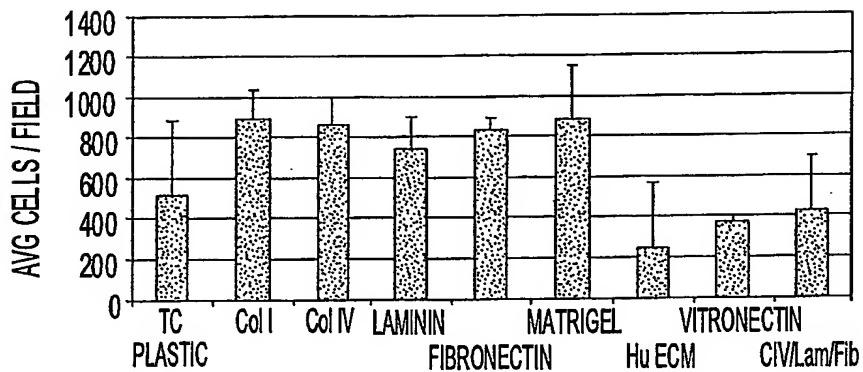


FIG. 4A

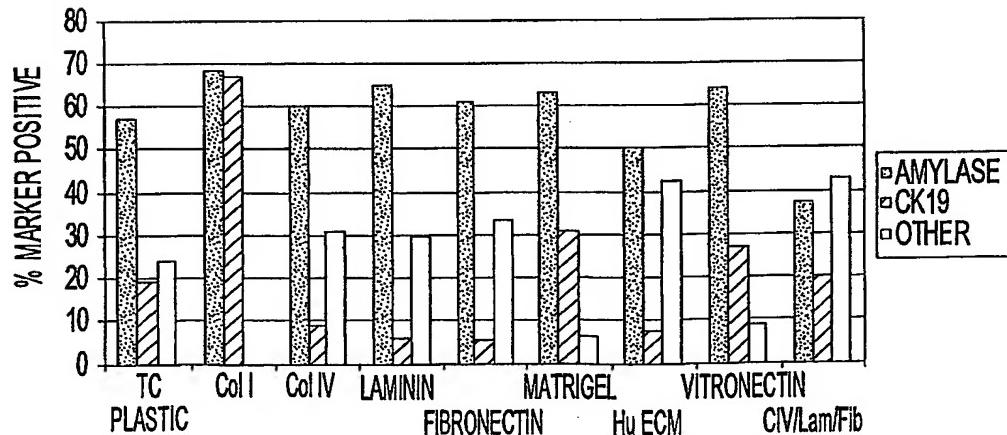


FIG. 4B

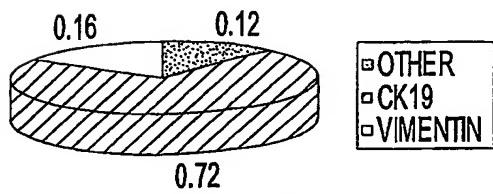


FIG. 5A

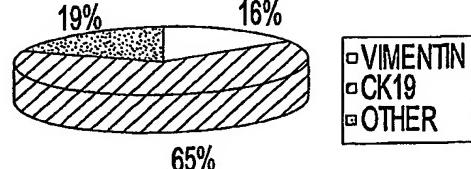


FIG. 5B

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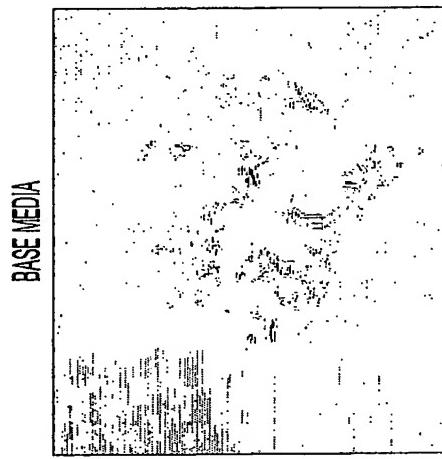


FIG. 6A

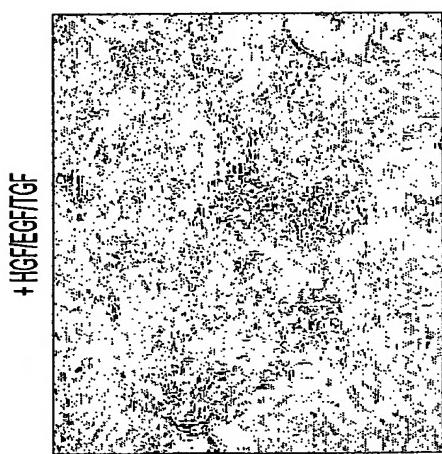


FIG. 6B

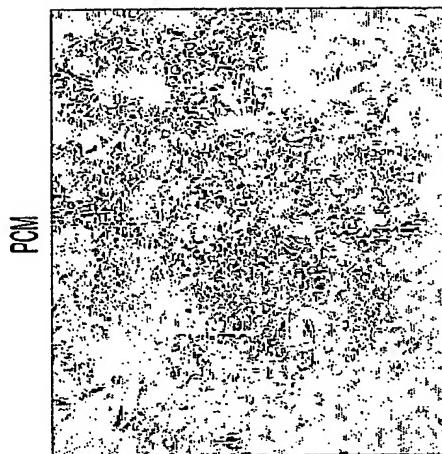


FIG. 6C

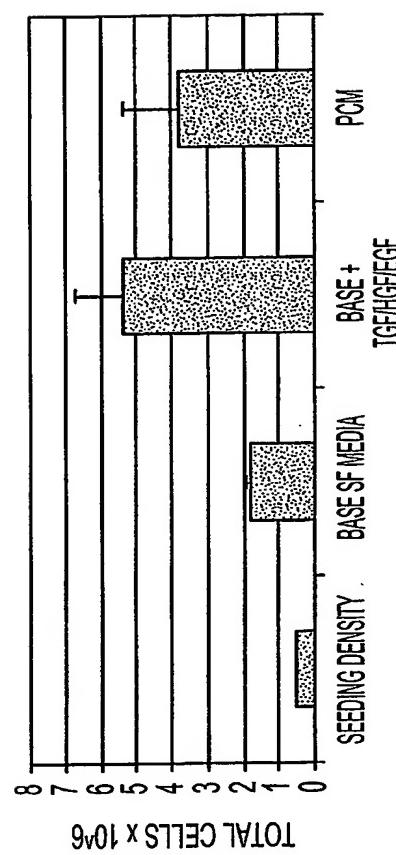


FIG. 6D

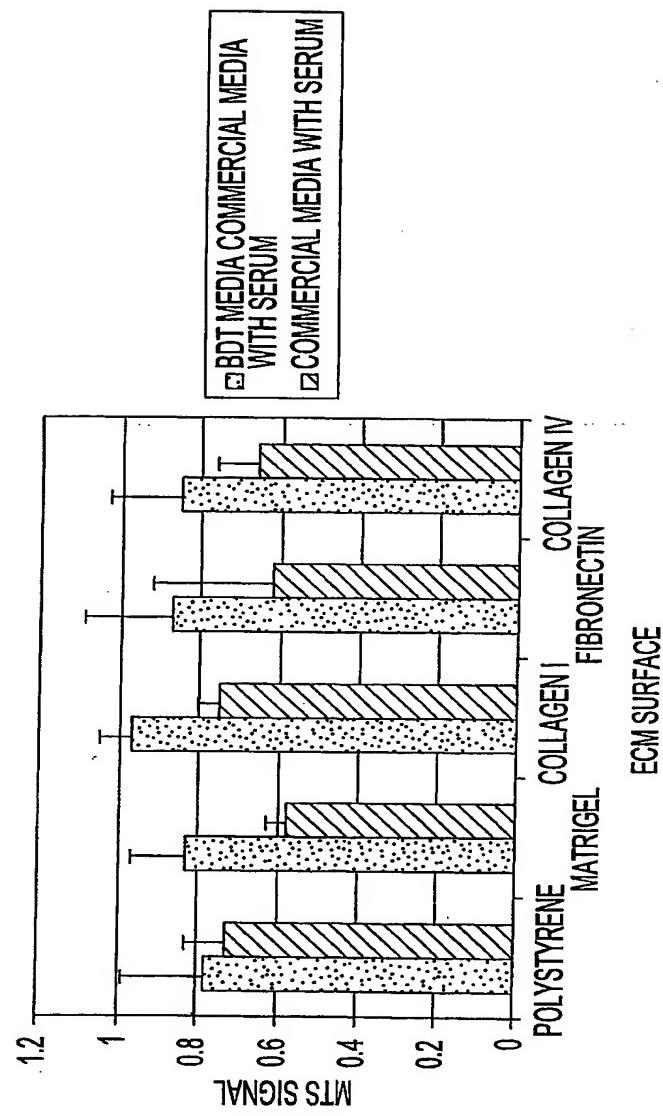


FIG. 7

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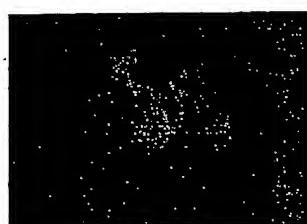


FIG. 8A



FIG. 8B

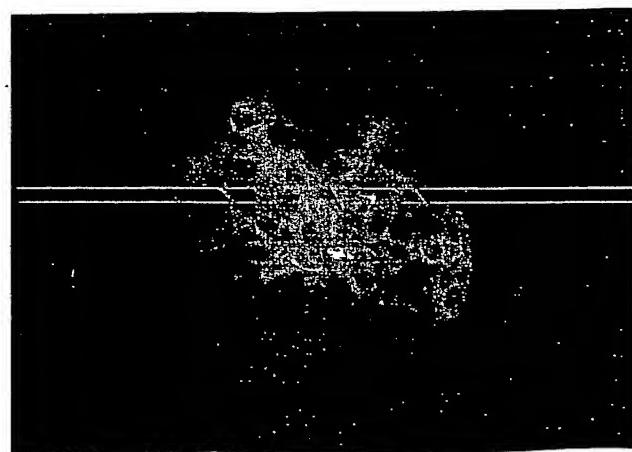


FIG. 8C

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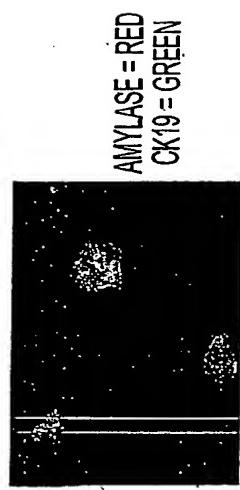


FIG. 9A

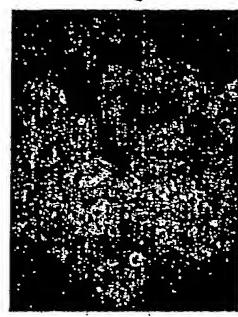


FIG. 9B

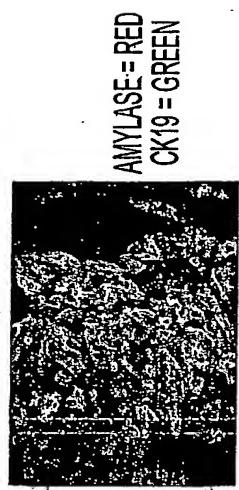


FIG. 9C

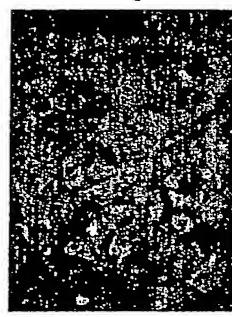


FIG. 9D

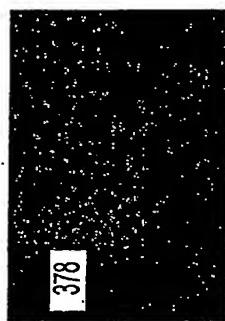


FIG. 10A

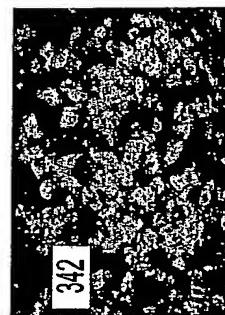


FIG. 10B

AMYLASE = RED  
CK19 = GREENAMYLASE = RED  
CK19 = GREENAMYLASE = RED  
CK19 = GREEN

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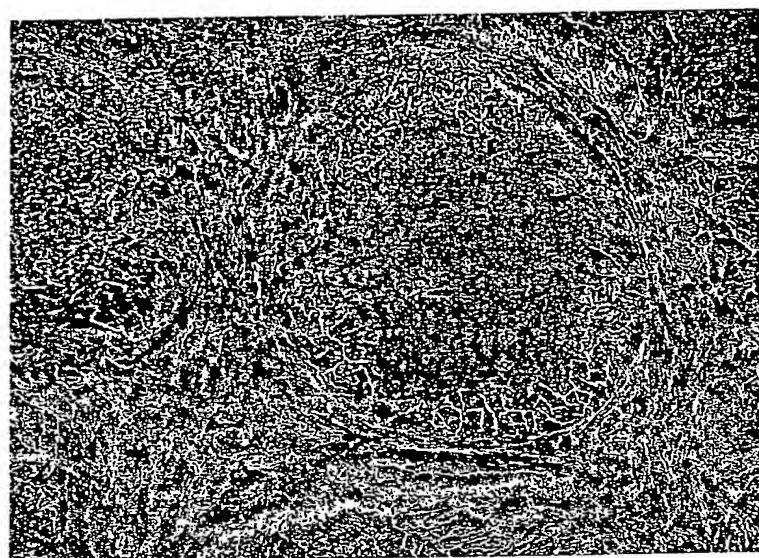


FIG. 11

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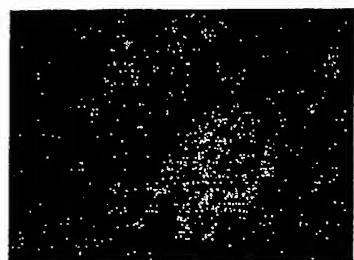


FIG. 12A



FIG. 12B

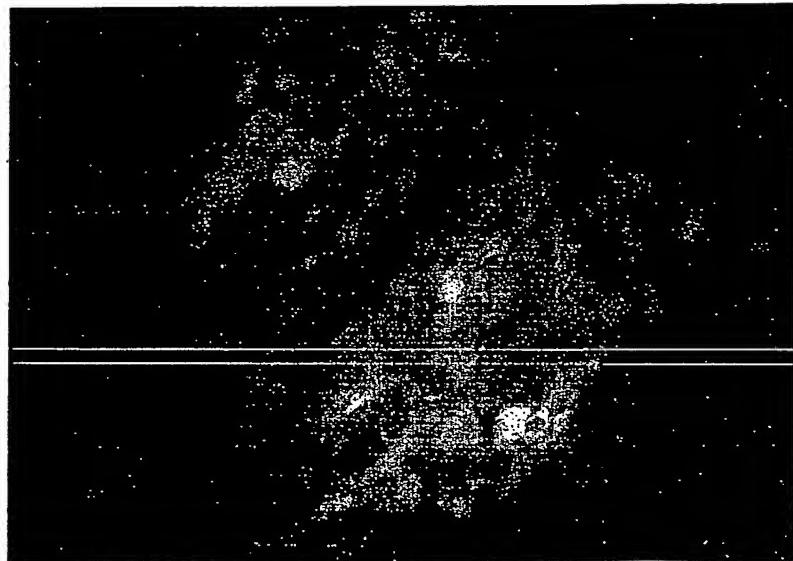
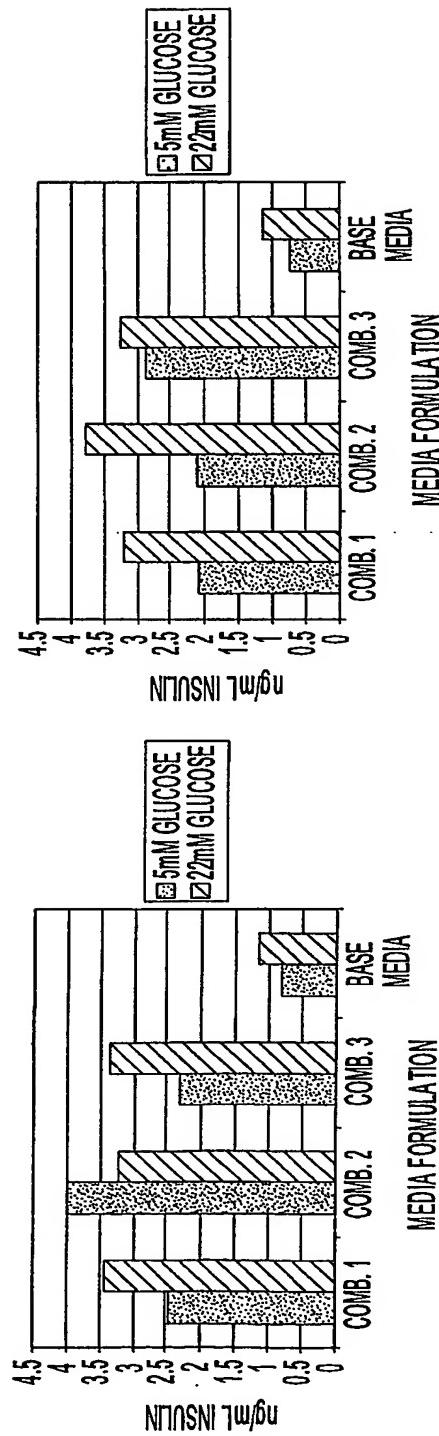
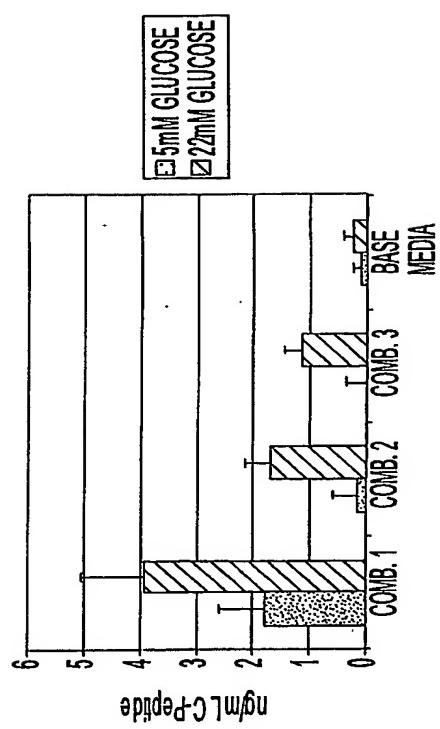


FIG. 12C

**FIG. 13B**

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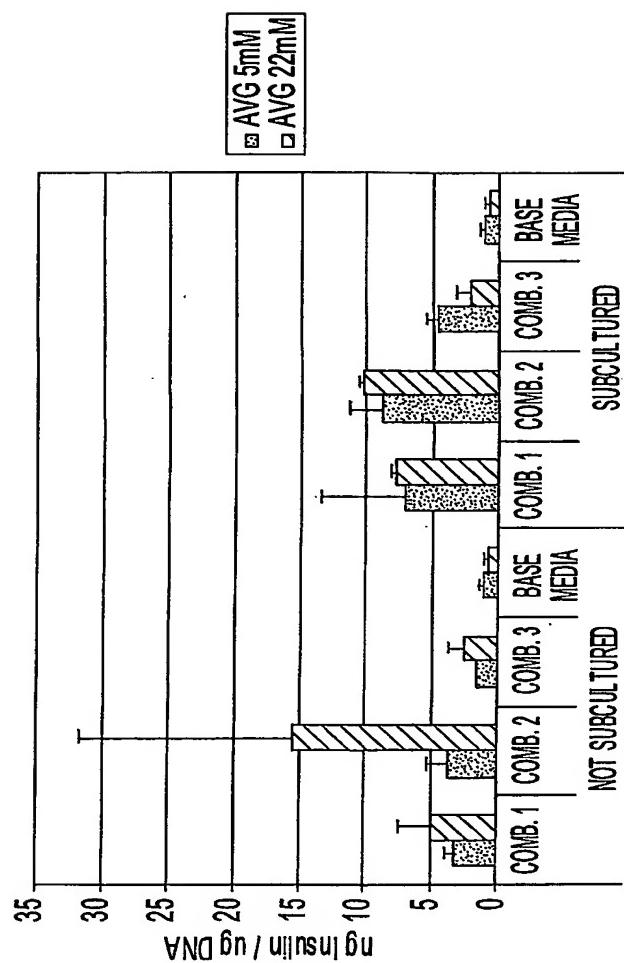


FIG. 14

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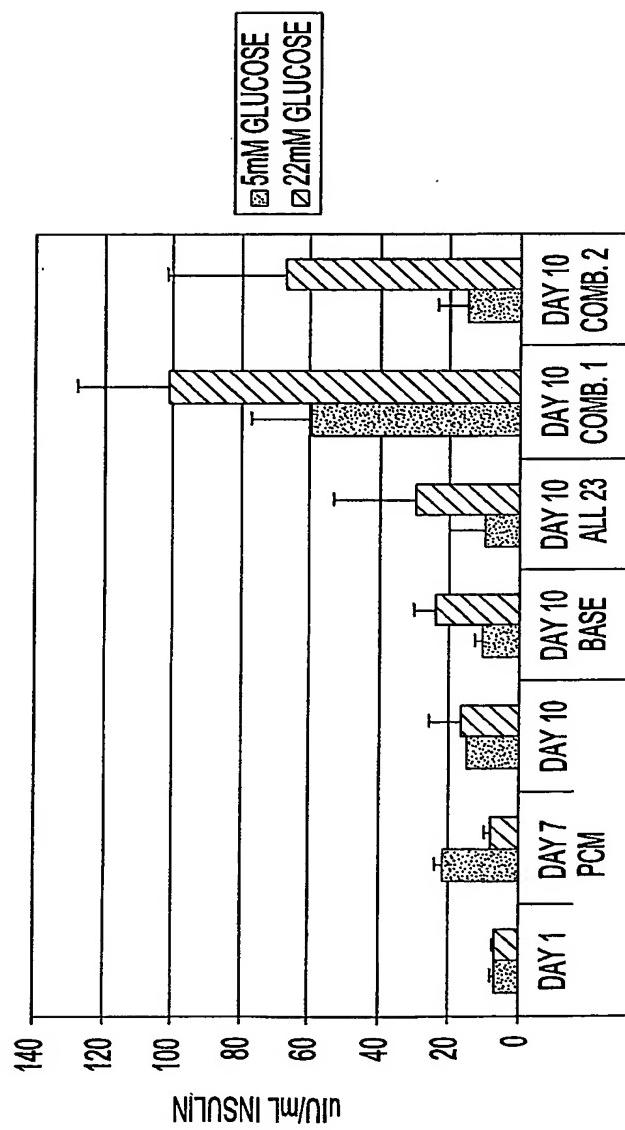


FIG. 15

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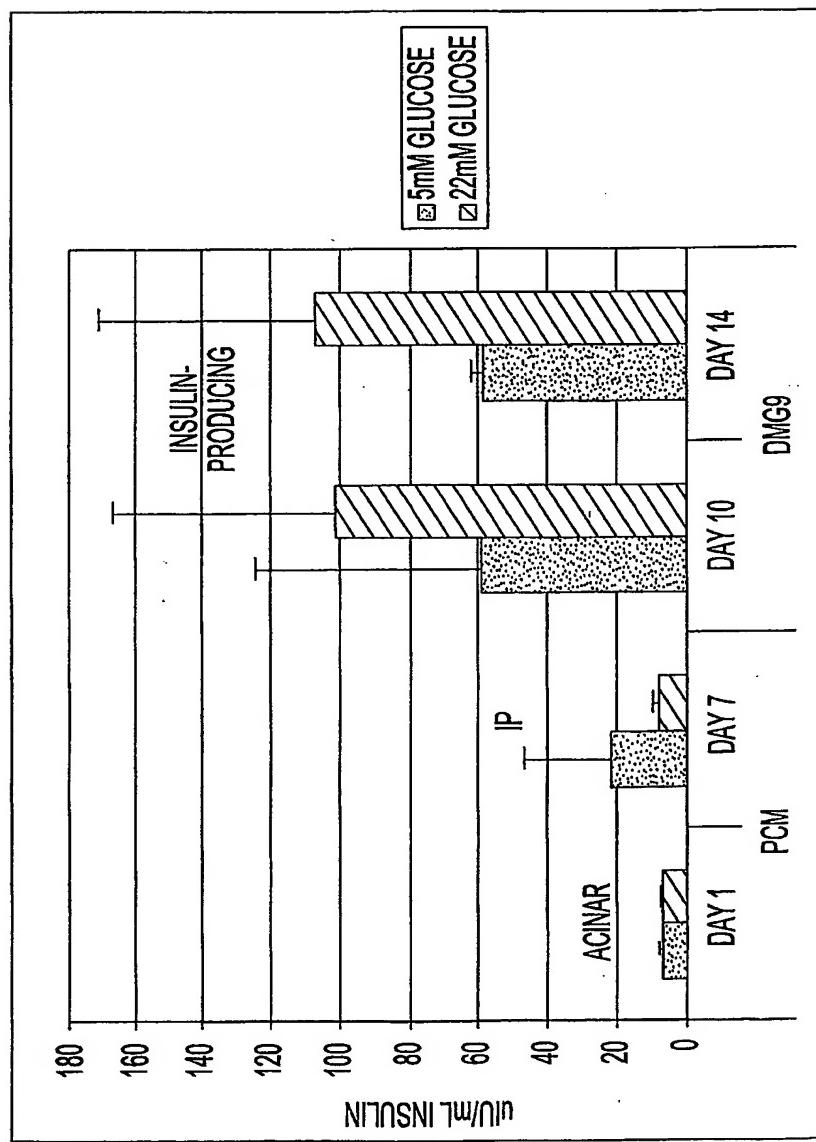


FIG. 15A

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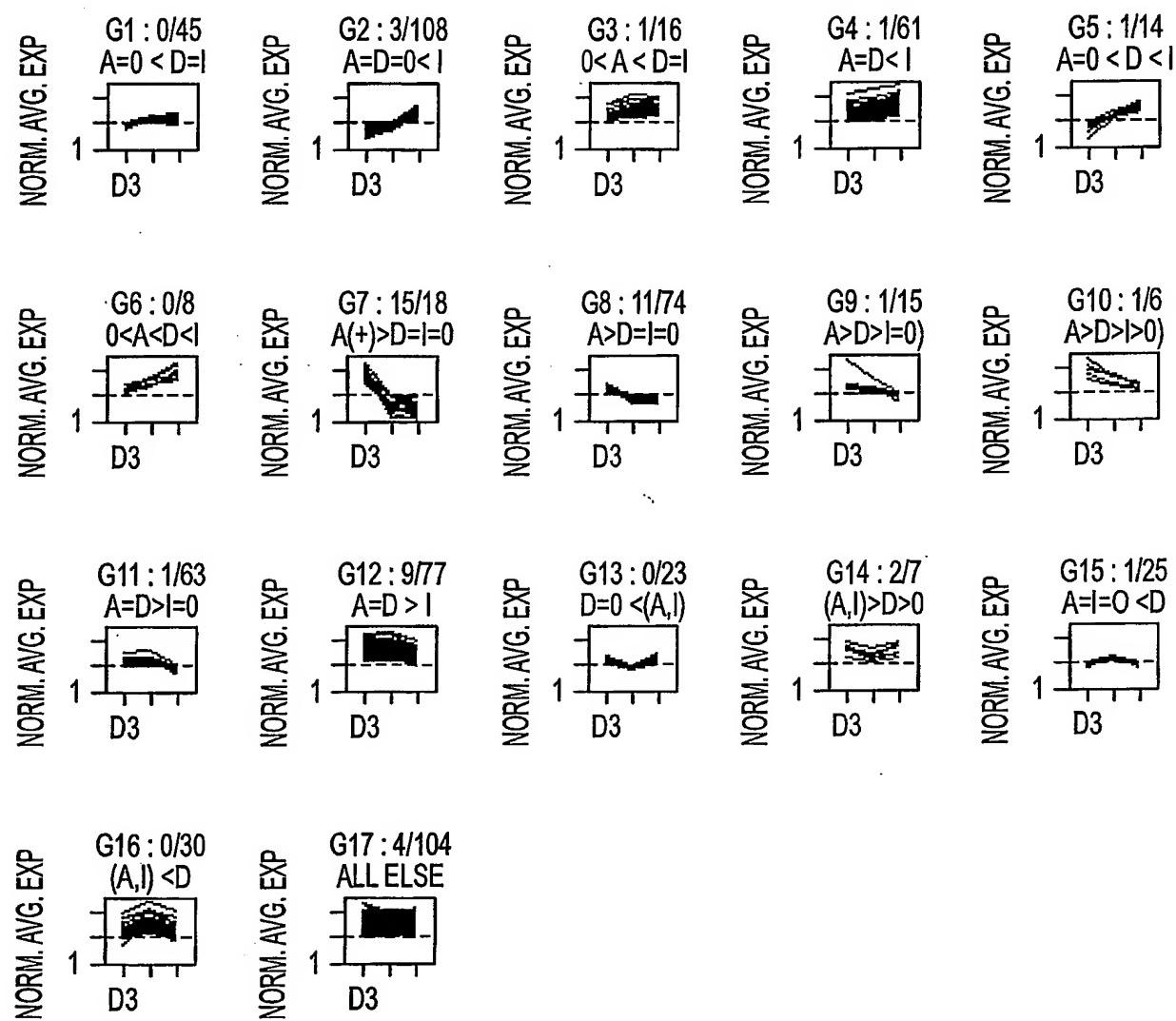


FIG. 16

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